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Fri Apr
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	April 1, 2004, 08:33:07; Search time 1398.42 Seconds (without alignments) 11033.514 Million cell updates/sec	US-09-727-855B-1 360xe: 3632 : 1 tcctgttgataatctttctaaagagcttgaaccattgtag 3632
	OM nucleic - nuc	Rum on:	Title: Perfect score: Sequence:

6747726 Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

IDENTITY_NUC Gapop 10.0

Scoring table:

Searched:

Minimum DB seg length: 0 Maximum DB.seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn1990s:*
geneseqn1990s:*
geneseqn2000s:*
geneseqn2001as:*
geneseqn2001as:*
geneseqn2002s:*
geneseqn2003s:* N_Geneseq_29Jan04:* 1: geneseqn1980s:* geneseqn2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	Aat85876 Malassezi		Abt33645 Anticance	Aaq70431 MHS:MnSOD	Abt 09580 Phase-1 R	Aaq53193 MnSOD cDN	Aat15589 Human man	Aat34277 Human man	Aax24998 Human nat	Aaa63891 cDNA enco	Abn84891 Human man	Aba94453 Human man	Ade76309 Human BSK	Abx63836 Human cDN	Abl66512 Lung canc	Abk84524 Human cDN	Aaq94284 Human man	Aaa75734 Nucleotid	Abk63720 Rat seque	Adb58236 Toxicity-	Aal26545 Human bre	Aad39690 Human MnS
	ID	AAT85876	ADD35245	ABT33645	AAQ70431	ABT09580	AAQ53193	AAT15589	AAT34277	AAX24998	AAA63891	ABN84891	ABA94453	ADE76309	ABX63836	ABL66512	ABK84524	AAQ94284	AAA75734	ABK63720	ADB58236	AAL26545	AAD39690
	DB	7	σ	7	7	9	7	N	N	7	ᠬ	9	9	σ	7	9	9	7	e	9	σ	4	9
	Length	728	897	270	627	999	813	813	813	813	813	849	849	930	972	1026	1026	1046	1438	1492	1492	2504	325
*	Query	2.3	2.2	2.0	2.0	2.0	7.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	7.0	2.0	2.0	2.0	2.0	2.0	2.0
	Score	84.2	78.8	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	73
	Result No.	1	7	e	4	Ŋ	G	7	80	6	1.0	11	12	13	14	15	16	17	18	19	20	21	22

Antigenic proteins from the fungus Malassezia - bind to IgE antibodies present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.

Kato I;

Onishi Y,

Kuroda M,

Yagihara T, I Yamaguchi H;

Takesako K, Okado T, Akiyama K, Yasueda H,

WPI; 1997-332788/30. P-PSDB; AAW29770.

The present sequence encodes a specifically claimed antigenic protein

Claim 53; Page 76-77; 162pp; Japanese.

Aac02178 Human sec

3 AAC02178

414

2.0

73

23

Abx49579 Bovine ES Aaz39779 Human man Aag20194 MnSOD (I Aag70432 MRS2:MnSO		Aag67474 Human man Aax33940 Human HCM Aax08429 Human man Abz83721 Toxicolog Aaz39782 Plasmid p Abx63709 Human cDN Aav31822 Mittant As	
ABX49579 AAZ39779 AAQ20194 AAQ70432	AAZ39781 AAN71370 AAN81158 AAT31018	AAQ67474 AAX33940 AAX08429 ABZ83721 AAX39782 ABX63709 AAV31822	AAZ20707 ABA93439 AAV73824 ABZ56304 AAF14076 ADB68898 ADB25718
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2 2 2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	. 330 310 310	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ρ 6 4 4 4 4 4 9 0 1 2 8 4 8

ALIGNMENTS

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Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody; allergy; antigen; ds.
                                                              Malassezia fungus MF-3 antigenic protein encoding cDNA.
                                                                                                               Location/Qualifiers
4. 621
/*tag= a /product= "MR-3_antigenic_protein"
            AAT85876 standard; cDNA to mRNA; 728 BP
                                                                                                                                                                              96WO-JP003602.
                                                                                                                                                                                                   96JP-00257612.
96JP-00257613.
                                                                                                                                                                                             95JP-00346627.
                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD
                                         (revised)
(first entry)
                                                                                                                                                                                           12-DEC-1995;
05-SEP-1996;
05-SEP-1996;
                                                                                                                                                                              10-DEC-1996;
                                                                                                                                                  WO9721817-A1
                                         27-AUG-2003
23-FEB-1998
                                                                                                                                                                19-JUN-1997
                                                                                                  Malassezia
                           AAT85876;
                                                                                                                Key
RESULT 1
      AAT85876
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1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.
                                                                                                                                                                                                                                                                                            50 Argogoriogagocorrrancionaagoagarcargacogrocacoacaagoagoca 109
                                                                                                                                                                                                                                                                                                                                                                          110 AGACCTACGTGAACAACCTCAACGCCGCCGAGAAGGCGTACGCTGAGGCGACGGCCGCGA 169
              IgE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be used in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
isolated from the fungus Malassezia. The antigenic protein can bind to
                                                                                                                                                                                                                                                       <u> AGACTTATGTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGG</u>
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; mouse; array; mitochondrial; hybridisation; energy-metabolism; mitochondrial disease; oxidative phosphorylation dysfunction;
                                                                                                                                                                                                                  ;
0
                                                                                                                                                                       2.3%; Score 84.2; DB 2; Length 728;
Larity 71.9%; Pred. No. 5.2e-14;
Conservative 0; Mismatches 43; Indels (
                                                                                                                                      Sequence 728 BP; 205 A; 204 C; 203 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                1425 AGGATGTGCTTACCCAGGTTAAGCTTCAGTCTG 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse mitochondrial DNA sequence SEQ ID NO:3025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 accacciócrinascacacacacacacacació 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 3025; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidative stress; apoptosis; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kerstann K,
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2001CA-02356540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD35245 standard; DNA; 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy S,
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                                                                                                                                                                                             Similarity
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31-AUG-2001;
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                                                                                                                                                                                                                  110;
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                                                                                                                                                                         Query Match
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produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid acid. The second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species, tissue and organisms, such organisms, which are useful for determining expression profiles diagnostic of energy metabolism-related physiological conditions, diagnostic such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, constitutions, and mutations involved in such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human conery metabolism-related physiological conditions. Evaluating and identifying animal models of human useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes one previously recognised to participate in mitochondrial DNA sequences shown in ADD33224-ADD35260 represent mutine mitochondrial DNA sequences shown in ADD33224-ADD35260 represent mutine mitochondrial DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA array, tumour; anticancer agent, drug tolerance factor; gene repair; nucleic acid metabolism; large-scale gene-expression profiling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 eccracerdaacaaccrcaaceccaceadaadaacraceadaecrcresccaagea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clones used to make the probes of the invention. Some sequences are present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 19
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; DB 9; Length 897;
2.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 897 BP; 225 A; 214 C; 247 G; 211 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anticancer agent target gene fragment SEQ ID No 49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azuma A, Fukushima M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%; Score 78.8; D 69.5%; Pred. No. 2.6e
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07-AUG-2001; 2001JP-00239181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                      tumour to an anticancer agent comprising at least thirteen different target gene fragments selected from at least two types of gene including genes for, enzymes associated with nucleic acid metabolism, gene repair, factors associated with drug tolerance, and housekeeping genes. The array assaying the sensitivity of tumours to anti-cancer agents. This polymucleotide sequence represents a target gene fragment of the
                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                 114 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 173
                                gene
                                                                           The invention relates to a novel DNA array for measuring sensitivity of
                                                                                                                                                                                                                                                          54 GCCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTGCACCACCACGAAGCACCACGCG
                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cosmetic; mutation;
inflammation; cancer;
                           expression of a number of different target sensitivity of tumors to anticancer agents.
                                                                                                                                                                                                Score 74; DB 7; Length 270; Pred. No. 3.2e-11; 0; Mismatches 50; Indels
                                                                                                                                                                             Sequence 270 BP; 72 A; 86 C; 66 G; 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
406 408
/*tag= b
/transl_except= pos:406 .408, aa:Gly
                                                                                                                                                                                                                                                                                                                    1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                    174 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manganese superoxide dismutase; MnSOD; oxygen;
arthritis; variant; enzyme; isoelectric point;
premature retinopathy; hypertension; diabetes;
                                                          Disclosure, Page 73; 83pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SIIT-) SII TECHNORESEARCH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92JP-00359959.
                                                                                                                                                                                                 2.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                           Best Local Similarity v...
Matches 104; Conservative
                             for measuring
for measuring
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          WPI; 2003-210360/20
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                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHS: MnSOD variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9414950-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1994
                           DNA array
                                      fragments
                                                                                                                                                           nvention.
                                                                                                                                                                                                                                                                                                                                                                                                          AAQ70431;
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acid substitution in a region which does not affect enzyme activity, of a positively charged amino acid residue, which has the effect of raising the isoelectric point of the peptide. These Mn-SoD variants are useful as medical prepns. for the treatment of human arthritis and diseases caused by active oxygen, and as cosmetic prepns. They are also useful for treatment of inflammation, cancer, premature retinopathy, hypertension and diabetes. Examples of variant Mn-SoDs are given in AAQ70431-32. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                           manganese super-oxide dismutase with aminoacid mutation in regions - for treatment of arthritis, active oxygen related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 165
                                                                                                                                                                                                                                                                                          Human variant manganese superoxide dismutase (Mn-SOD) comprises an amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; toxicity study; rat toxic response gene; toxicological response;
drug development; phase-1 rat CT gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 627 BP; 175 A; 152 C; 160 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 2; Length 627
Pred. No. 5.6e-11;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 GATGITACAGCCCAGATAGCTCTTCAGCCTGCAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                             Example 3; Page 16-17; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CT gene SEQ ID No 668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
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                                                                                                                          non-essential regions - for disorders and for cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%;
Best Local Similarity 67.5%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2002; 2002WO-US002935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2001; 2001US-0264933P.
26-JUL-2001; 2001US-0308161P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response to the test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farris G, Hicken SH,
WPI; 1994-234688/28.
P-PSDB; AAR60360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-674961/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT09580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200266682-A2
                                                                                           Human variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phase-1 Rat
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ABT09580
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WPI; 1996-059735/07.
P-PSDB; AAR90713.
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Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1987;
inflammation
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06-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIATGITAACGGCCTCAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 Accthochtohacharchdadcercaccadadadadanchacacadadceridecchadada 243
                                                                         agent comprising determining the expression of a rat toxic response gene(s) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion; injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
                                                       invention relates to a method used for evaluating the toxicity of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCACCACCACCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression plasmid in Escherichia coli host system - encodes human manganese superoxidedismutase analogue, useful for e.g. treating
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 6; Length 666;
Pred. No. 5.9e-11;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                              Sequence 666 BP; 172 A; 164 C; 182 G; 146 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gargiracaacrcaggirgcrciricagccrcad
     Disclosure; Page 270; 388pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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86IE-00002851.
87US-00032734.
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                                                                                                                                                                                                                                                                                                                                                                         2.0%;
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5270195-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                           104;
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Matches
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                                          The sequence encodes a maganese superoxide dismutase which can be used to catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide and molecular oxygen. It can be used to reduce reperfusion injury following ischaemia and prolong the survival of excised organs. It can also me used as a long acting anti-inflamatory drug. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                      GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 gecerganacerenchrenaegegechentenegengergenechenaennageneege
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Manganese superoxide-dismutase"
note= "EC-1.15.1.1"
                                                                                                                                                                                                                                     Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             Length 813;
                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                             Score 74; DB 2;
Pred. No. 6.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGITACAGCCCAGATAGCTCTTCAGCCTGCAC 304
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human manganese superoxide-dismutase cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Claim 1; Fig la-1c; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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88US-00161117
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115. .708
/*tag= c
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                                                                         Hartman JR, Beck Y;
                                                                                                  WPI; 1996-361912/36.
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                             P-PSDB; AAW00018
 13-DEC-1989;
10-JUL-1992;
14-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104;
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                                                                                         has been isolated from a human T-lymphocyte cDNA library in phage lambdagel in Escherichia coli, by screening with a 5-probe (AATI5591) and a 3'-probe (AATI5592). The sequence of the insert in plasmid ph88-4 (obtained by subcloning in plasmid pB83-22) is shown. The cDNA may be expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD product may be cleaved with Aeromonas proteclytica aminopeptidase to pistidine residues removed. The MnSOD analogue with lysine and optionally histidine residues removed. The MnSOD analogue with lysine and optionally conditions associated with generation of oxygen free radicals, particularly synovial inflammation, arthritis and lung fibrosis (claimed). (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                                                                                                                                                                                            211 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 270
           New human manganese super:oxide dismutase analogues - having a Lys and opt. His residue absent from the N-terminus, useful for treating e.g. synovial inflammation, arthritis or lung fibrosis.
                                                                                                                                                                                                                                                                                                                                         Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia; bronchial pulmonary dysplasia; inflammation; antiinflammatory; ds.
                                                                                 The sequence encodes a human manganese superoxide-dismutase (MnSOD),
                                                                                                                                                                                                                                                      Best Local Similarity 67.5%; Score 74; DB 2; Length 813; Matches 104; Conservative 0; Mismatche-
                                                                                                                                                                                                                                          Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                          271 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human manganese superoxide dismutase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                                                          Example 1; Fig 1; 45pp; English
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86US-00907051.
86IE-0002851.
87US-00032734.
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29-OCT-1986;
27-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                               A cDNA clone (AAT34277) codes for human manganese superoxide dismutase (MnSOD) (AAW00018), an enzyme that catalyges the reduction of superoxide radicals to H2O2 and 02. It was isolated from a human T - cell library cloned into vector g100 using probes (see also AAT34283- 84) based on portions of mature MnSOD. The MnSOD gene was also identified (see also AAT34278-82). The cDNA can be used for the prodn. of recombinant MnSOD using e.g. Escherichia coll cells as hosts. The MnSOD is useful for reducing reperfusion injury, treating inflammation or bronchial pulmonary dysplasia and for prolonging survival of excised organs. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 270
                                                                                                                                                                                                                                                                                 Jse of recombinant human manganese super:oxide dismutase - for treating inflammation or bronchial pulmonary dysplasia, reducing reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GCCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTGCACCACCACGAGCACCACGCG
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Pred. No. 6.7e-11;
0; Mismatches 50;
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                                                                                                   (BIOT-) BIO-TECHNOLOGY GENERAL CORP
                                                                                                                                                                                                                                                                                                                                      injury or prolonging organ survival
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89US-00453057.
92US-00912213.
93US-00120951.
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Silverman DN,
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                                                                                                               sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA sequence codes for human manganese superoxide dismutase
(hwm.SOD, see AAW98169). Novel MnSOD proteins having catalytic activity
which differs from this natural hum.SOD are claimed. The modified proceins
exhibit reduced or no product inhibition, or have greater activity, or
both, compared to natural hum.SOD. The modifications involve one or amino
acid substitutions within the active site of the enzyme, especially at
residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
His-163 (see also AAW98171-77). Nucleic acids encoding the modified and
hum.SOD proteins are also claimed. The modified hum.SOD proteins, or
cypresidue the which modified hum.SOD nucleic acids is linked to a
promoter (preferably mammalian), can be used to protect a cell linke from
damage caused by superoxide radicals (claimed). They can also be used to
treat subjects suffering from, or at risk of, cytotoxicity caused by
superoxide radicals (claimed) As such, they can be used as antioxidants
in the treatment of a variety of disorders, including inflammation
(claimed), reperfusion injury following ischemia (claimed), and cellular
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                                                                                                                                                                                                                                                                                                                         New recombinant human manganese superoxide dismutase proteins
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Pred. No. 6.7e-11;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding a human manganese superoxide dismutase.
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Matches 104; Conservative
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                                                                                                                                                                                                               Nick HS, Silverman DN;
                                                                                                                                                                 (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                          WPI; 1999-229242/19.
                                                                                                                                                                                                                                                                                P-PSDE; AAW98169
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                        18-MAR-1999
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1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAG 1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human manganese superoxide dismutase protein (hwn SOD). The specification describes a medified hwn SOD which has a catalytic activity which differs from natural hwn SOD in that it exhibits reduced or no product inhibition compared to natural hwn SOD. The natural hwn SOD is especially modified with one or more substitutions in amino acids 26, 30, 34, 74, 143, 159, 161 and 163. The modified hwn SOD is useful for protecting a cell from damage caused by superoxide radicals and for treating a cell from damage caused by superoxide radicals. The protein is useful for treating inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human manganese superoxide dismutase protein useful as antioxidant for treating cytotoxicity caused by superoxide radicals, inflammation and reperfusion injury following ischemia.
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0
                          /transl_except= (pos: 505. .507, aa: Xaa)
/transl_except= (pos: 511. .513, aa: Ala)
/product= "manganese superoxide dismutase"
/note= "Xaa is Gln or Glu"
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Pred. No. 6.7e-11;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human manganese superoxide dismutase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reperfusion injury following ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 25-26; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN84891 standard; cDNA; 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00151052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00927230.
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Local Similarity 67.5%;
                                                                                                                                                                              43. .114
/*tag= b
115. .708
/*tag= c
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/*tag=
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Treating inflammatory joint disease such as osteoarthritis, rheumatoid arthritis and post ischemic tissue injury, comprises injecting human manganese superoxide dismutase.
                                                                                              Human manganese superoxide dismutase; antiinflammatory; antiarthritic; antirheumatic; vasotropic; osteopathic; hSODm; human; ss.
                                                             Human manganese superoxide dismutase (hSODm) encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mullenbach GT;
                                                                                                                                                                               Location/Qualifiers
100. .768
                                                                                                                                                                                                                               "hSODm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 4; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               86US-00918534.
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/product= 100..171
                              (first entry)
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172..765
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                                                                                                                                                                                                                                                                             172...7
/*tag=
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P-PSDB; ABB07330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1986;
                              09-APR-2002
                                                                                                                                                                                                                                                                                                                             JS6326003-B1
                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                               mat_peptide
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ABA94453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the nucleotide sequence of human manganese supercoxide dismurase (hSODM) cDNA. The cDNA was isolated from an adult human kidney cDNA library in lambda-gt10 using the probes given in ABN84889-90. The invention relates to methods for hSODM gene cloning and expression in microorganisms, especially Escherichia coli or Saccharomyces cerevitates. The hSODM cDNA is inserted into a vector for expression in the microbial host, preferably under conditions which allow for processing to remove the N-terminal methionine. The expression product is useful for treating a patient having inflammancory joint disease (e.g. osteoarthritis or rheumatoid arthritis), or to minimise post-ischaemic tissue damage resulting from disease or surgery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing recombinant human manganese superoxide dismutase, useful in the treatment of osteoarthritis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 GCCTACGTGAACAACCTGAACGTCACCGAGGAGGAGTACCAGGAGGCGTTGGCCAAGGGA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCACCAAGCACCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 GCCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTGCACCACACAAGCAACCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 849;
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Pred. No. 6.9e-11;
0; Mismatches 50; Indels
                                                                 /*tag= a
/rote= "EcoRI linker used in cloning"
                                                                                                                                                                                                                                                          /note= "EcoRI linker used in cloning"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mullenbach GT;
                                         Location/Qualifiers
                                                                                                                                           "hSODm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 4; 16pp; English
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/product=
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172. .765
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842. .849
                                                                                                                                                            .171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bell GI,
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P-PSDB; ABB79798.
                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP
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Best Local Similarity
                                                                                                                                                                                                                                                                                             US2002081287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallewell RA,
             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          11-JUN-2001;
                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1986;
                                                                                                                                                                                                                             misc feature
                                                                                                                                                            sig_peptide
                                                                                                                                                                                            mat_peptide
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ID ABA9
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The invention relates to a method of treating a patient with inflammatory joint disease. The method involves intra-articularly injecting into the afflicted joint a solution of human manganese superoxide dismutase (hSODm). The treatment is used to treat an inflammatory joint disease, particularly osteoarthritis or rheumatoid arthritis. The method can also be used to treat post isohemic tissue injury. The present sequence represents a CDNA encoding the hSODm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 GCCTACGTGAACATCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                   Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        2.0%; Score 74; DB 6; Length 849; 67.5%; Pred. No. 6.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                            50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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ADE76309
ID ADE76
XX
AC ADE76
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ABA94453 standard; cDNA; 849 BP

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d à 26-FEB-2003 (first entry)

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monocyte; macrophage; gene expression profile; rheumatoid arthritis; chronic inflammatory disease; bacteria-induced inflammation; arteriosclerosis; tumour; organ; tissue transplant; sepsis; molecular classification; human; BSK; ss.
                     Human BSK-1H13 complementary strand DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX63836 standard; cDNA; 972
                                                                                                            02-OCT-2002; 2002EP-00090348.
                                                                                                                          09-NOV-2001; 2001DE-01055600.
       (first entry)
                                                                                                                                        (OLIG-) OLIGENE GMBH.
                                                                     Homo sapiens
                                                                                  EP1310567-A2
       29-JAN-2004
                                                                                               14-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX63836;
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monitoring of therapy having, on its surface, sequences of some or all of monitoring of therapy having, on its surface, sequences of some or all of specified monocyte-macrophage genes and also of other genes or RNA complementary to the specified genes. The device of the invention may be used to determine gene expression profiles for measurement of monocyte or macrophage activation or inflammation in blood or other tissues, as well set for the diagnosis, prognosis and monitoring therapy in cases of theumatoid arbritis, chronic inflammatory disease, chronic bacteriatinduced inflammation, arteriosclerosis, tumours, organ or tissue classification and sepais. The device provides information for molecular classification and staging of disease, creation of a patient-specific prognostic profile and suggestions about molecular pathogenesis or therapeutic effects, thus facilitating the development of new therapeutic the human RKX DNA of the invention 0 1367 ACTIAIGITAACGGCCTCAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426 Device for diagnosis, prognosis and monitoring therapy of e.g. rheumatoid arthritis, comprises immobilized gene sequences from monocyte-macrophage 67 decengdaacencaeareaaegeegagareargeagergeaeergeaeeaegageaeege 126 127 gecriacergaacarcergaacercaeceaegaagaagraecaegageegriegecaagega 186 .; 0 Sequence 930 BP; 242 A; 208 C; 206 G; 245 T; 0 U; 29 Other; 2.0%; Score 74; DB 9; Length 930; 67.5%; Pred. No. 7.4e-11; 50; Indels GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460 187 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 220 0; Mismatches Claim 29; SEQ ID NO 121; 180pp; German. human BSK DNA of the invention. Stuhlmueller B, Haeupl T; Matches 104; Conservative WPI; 2003-443090/42. Local Similarity

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This invention relates to a combination comprising several CDNAs that are disferentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed companies. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; cynaecological; vasotropic and cerebroprofective activities and may be used in gene therapy. The CDNAs of the invention may be used in gene therapy. The CDNAs of the invention may be used in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a CDNA of the invention. A protein encoded by the CDNA may be used to screen several contents or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample. The nucleotides may be useful for recombinant protein from a sample. The nucleotides may be useful for diagnosing, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosoclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischeemia reperfusion conjury, restension, diabetes, pre-eclampsia, ischeemia reperfusion conjury, restension, diabetes, pre-eclampsia, ischeemia reperfusion conjury, restension, diabetes, pre-eclampsia, ischeemia caid caid associated with abnormalities in the expression, amount or aute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention content is adifferentially expressed in activated vascular tissue. Note: The content of the specification, but the content of the specification, but the content of the sequence data for this patent did of form to the protein the detection of the protein contents of the sequence data for this patent did detectly from used for the protein contents of the specification, and directly from the contents of th
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                                                                                             Human, gene, ss; vascular tissue, cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasctropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hyportension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 GOCCTGGAACCTCACATCAAGGCGCAGATCATGCAGCTGCACCACGCAAGCACCACGCG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated
                                              Human cDNA #836 differentially expressed in activated vascular tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000US-0222469P. 08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 18pp; English.
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GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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                    (AVAL-) AVALON PHARM
                                                                   WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April Job time: 1407.42 secs
                                  Young PE, I
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1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
           262 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 321
                                                                                                                                                                                            stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                Lung cancer related gene sequence SEQ ID NO:4849.
                                     1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                   ABL66512 standard; DNA; 1026 BP
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2000US-0235814P

2000US-0235880P

2000US-023583P

2000US-023563P

2000US-023572P

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2000US-0237295P.
2000US-0237316P.
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2000US-0237608P.
2000US-0244867P.
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                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                   WO200194629-A2.
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25-SEP-2000; 2
25-SEP-2000; 2
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26-SEP-2000;
27-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
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20-SEP-2000;
20-SEP-2000;
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25-SEP-2000;
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28-SEP-2000;
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                                                                                                                          ABL66512;
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                                                                                              ABL66512
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The present invention describes a method (M1) for screening for an anti-
neoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
comprises a sequence (S) selected from 847 sequences (given in ABL61664
comprises a sequence (S) selected from 847 sequences (given in ABL61664
comprises a sequence (S) selected from 847 sequences (given in ABL61664
comprises a sequence (S) selected from 847 sequences (I)
activity and can be used in the incoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. MI can be used for screening an
anti-neoplastic agent, and can be used for producing a product which is
the data collected with respect to the anti-neoplastic agent as a result
of MI, and the data is sufficient to convey the chemical structure and/or
properties of the agent. MI can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
prostate or pancreatic cancer, adenome, clear cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Milm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1367 ACTIAIGITAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 232
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Pred. No. 7.9e-11;
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01-NOV-2000; 2000US-0245084P.
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Best Local Similarity 67.53
Matches 104, Conservative
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Weaver Z;
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April 1, 2004, 12:34:16; Search time 1266.68 Seconds (without alignments) 10723.022 Million cell updates/sec
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2. \cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

3. \cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 25, Appl	Sequence 122, App	Sequence 24298, A	Sequence 4. Appli	Sequence 3227, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 29, Appl	Sequence 2, Appli	Seguence 267, App	Sequence 90403, A	Sequence 1077, Ap	Sequence 715, App	Sequence 1059, Ap	Sequence 23123, A		Sequence 32727, A	Seguence 67, Appl	Sequence 16177, A	Sequence 9423, Ap	Sequence 90405, A	Sequence 13, Appl	Sequence 6456, Ap	Sequence 5724, Ap	Sequence 5493, Ap	Sequence 294, App	Sequence 2105, Ap	Sequence 9, Appli	Sequence 4529, Ap	Sequence 11115, A
	14 US-10-247-671-122	10 US-09-918-995-24298	14 US-10-109-670-4	9 US-09-738-626-3227	9 US-09-818-564-1	9 US-09-738-626-1	14 US-10-109-670-29	9 US-09-727-855B-2	12 US-10-342-887-267	12 US-10-424-599-90403	10 US-09-960-706-1077	10 US-09-873-319-715	10 US-09-873-367C-1059		12 US-10-085-783A-32727	15 US-10-242-535A-32727	9 US-09-920-455-67		14 US-10-029-386-9423		9 US-09-960-352-13	9 US-09-960-352-6456	9 US-09-960-352-5724	9 US-09-960-352-5493		11 US-09-864-408A-2105	14 US-10-230-331-9	9 US-09-960-352-4529	9 US-09-960-352-11115
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1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.7	1.7	1.6	1.6	1.6	1.6	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
9.89	68.2	67.8	66.2	65.2	65.2	65.2	63.6	60.8	60.4	59	56.8	56.8	56.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	52.6	52.6	52.6	52.6	52.6	51.8	51.8	51	51
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ALIGNMENTS

RESULT 1 US-09-727-855B-1 USEFUI

Sequence I. Application US/09727855B Sequence I. Application US/09727855B Sequence I. Application US/09727855B GENERAL INFORMATION. APPLICANT: HOSHINO, Tatsuo APPLICANT: OJIMA, KAZUAJUAI APPLICANT: OJIMA, KAZUAJUAI APPLICANT: OJIMA, KAZUAJUAI APPLICANT: OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY TITLE OF INVENTION: MAPERIALS THEREOF FILE REFERENCE: C38435/111694 CURRENT APPLICATION NUMBER: US/09/727,855B CURRENT APPLICATION NUMBER: US/09/727,855B NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 EIGHGHI 3632 EIGHGHI 3632 TYPE: DNA ORGANISM: Phaffia rhodozyma	Query Match 100.0%; Score 3632; DB 9; Length 3632; Best Local Similarity 100.0%; Pred. No. 0; Matches 3632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TCCTGTTGATAATCTTTCTAACGCCTTGTACTTTGACCAAGGCGTTTGTCCGAAATTTTG 60 	CAAACTTAGTGTTGGTCGATGGACGGTCTTCGGATCCAGAACTGACGGCTCGCCAATAA 120 	AGTATGACGATGGTAGAGGTGAAGGAGGGAACCACAGGTTGACCAGTCTCAAAGAGTGCT 180 	GATGTGCGCGAGGATTTGTCATTAAATGGTGTTGTATATGCTAGAGCCAAGAGAAGACAT 240
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RESULT 2
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Sequence 4, Application US/09727855B
Sequence 4, Application US/09727855B
Sequence 4, Application US/09727855B
Sequence 4, Application US/09727855B
Sequence 6, US20020168703A1
GENERAL INFORMATION:
APPLICANT: HOSHINO, TATAKA
APPLICANT: SETOGUCHI, YULAKA
TITLE OF INVENTION: MATERIALS THEREOF
TITLE OF INVENTION: MATERIALS THEREOF
CURRENT APPLICATION NUMBER: US/09/727, 855B
CURRENT APPLICATION NUMBER: US/09/727, 855B
CURRENT FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
CTCGGGCTCGTAGATGCTGATGAAACACAATAGGTAGTAGGAGGAGGAGAAAGAGAAGATG 3540
                                                                                                   3541 ATGAGATGTCAGGATGCTTCACTGTAGATGGAGGAAGAAGATATGCGAAGCAAGAC 3600
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                                     3481 CTCGGGCTCGTAGATGCTGATGAACACAATAGGTAGTÄGGAGAGAGAGAAAAGATG 3540
                                                                               3541 ATGAGATGTCAGGATGCTTGCTTCACTGTAGATGGAGGAAGATATGCGAAGCAAGAC
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Sequence 3, Application US/10109670

Sequence 3, Application US/10109670

Sequence 3, Application US/10109670

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH et al.

TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA

FILE REFERENCE: 142-0553P

CURRENT APPLICATION NUMBER: US/10/109,670

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 58
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Pred. No. 9.7e-36;
0; Mismatches 1;
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ORGANISM: Malassezia furfur
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ORGANISM: Phaffia rhodozyma
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NAME/KEY: misc_feature
LOCATION: (1)..(728)
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Best Local Similarity
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               ACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGACTATCTCGCTGCTGTTTGGTCCG
                                            TTATCAACTACAAGGAGGCAGAGGCCCGATTGCAGGCTGCTCTCTAAGCGGGACGAAAAG
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JAPELICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR PELLOR DATE: 2001-09-18
PRIOR PELLOR DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR PLILNG DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/234,923
PRIOR PLILNG DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PLILNG DATE: 2000-09-25
PRIOR PLILNG DATE: 2000-09-26
PRIOR PLILNG DATE: 2000-09-26
PRIOR PLILNG DATE: 2000-09-26
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PRIOR PLILNG DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
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Pred, No. 2.2e-11;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                 Score 74; DB 14; Length 99
Pred. No. 2.1e-11;
0; Mismatches 50; Indels
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         PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13503
LENGTH: 996
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Patent No. US20020115057A1
GENERAL INFORMATION:
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Best Local Similarity 67.5%;
Matches 104; Conservative (
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CORGANISM: Homo sapiens
US-09-954-456-1822
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US-10-198-846-13503
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Best Local Similarity
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US-09-954-456-1822
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; OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
US-10-109-670-3
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 816
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APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAFY OF BREAST CANCER
FILE RFFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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                                                                                                                Length 728;
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                                                                                                             Score 84.2; DB 14; Length Pred. No. 1.1e-14; 0; Mismatches 43; Indels
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US-10-044-090-836
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nilarity 71.9%;
Conservative 0
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ORGANISM: Homo sapiens
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                                                                                                         Query Match
Best Local Similarity
Matches 110; Conserva
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US-10-198-846-13503
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US-10-044-090-836
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Query Match
Best Local Similarity 67.5;
Matches 104; Conservative
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CNGANISM: Homo sapiens
US-10-342-887-1905
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ORGANISM: Homo sapiens
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LENGTH: 1067
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                                       173 GCCTACGTGAACAACCTGAACGTCACGGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 232
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van (* Veer, Laura Johanna
APPLICANT: Van (* Viver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-188-999 CURRENT APPLICATION NUMBER: US/10/342,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; DB 12; Length 1026;
Pred. No. 2.2e-11;
0; Mismatches 50; Indels
                                                                                 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/298,918
PRIOR PELING DATE: 2003-01-15
PRIOR FILING DATE: 2001-06-18
PRIOR PELICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-06-14
PRIOR PELICATION NUMBER: 10/172,118
PRIOR PELING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
LENGTH. 2003-06-14
LENGTH. 2003-06-14
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Publication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linaley, Peter S.
APPLICANT: Anolyme
APPLICANT: Anolyme
APPLICANT: Roberts, Christopher J.
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Van de Vijver, Marc J.
Bernards, Rene
                                                                                                                                                                                                                            Sequence 509, Application US/10342887
Publication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
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Best Local Similarity 67.5%;
Matches 104; Conservative
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CORGANISM: Homo sapiens
US-10-342-887-509
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US-10-342-887-1905
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1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAG 1366
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Pred. No. 2.2e-11;
0; Mismatches 50; Indels
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; OTHER INFORMATION: Incyte ID No. US20030175704A1 241107.19
US-09-971-429B-22
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US-09-971-429B-22
Sequence 22, Application US/09971429B
Publication No. US20030175704A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy K. W.
APPLICANT: Bhyjan, Andrew W.
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: GREES EXPRESSED IN LUNG CANCER
FILE REFERENCE: PA-0040 US
CURRENT APPLICATION NUMBER: US/09/971,429B
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGram
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Pred. No. 2.2e-11;
0; Mismatches 50
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CURRENT FILING DATE: 2003-01-15

PRIOR PELLING DATE: 2001-05

PRIOR FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 60/380,710

PRIOR PILING DATE: 2002-05-14

PRIOR PILING DATE: 2002-05-14

PRIOR PILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 1905

LENGTH: 1026
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Best Local Similarity 67.5%;
Matches 104; Conservative
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CURRENT APPLICATION NUMBER: US/10/198,846
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US-09-960-352-14744
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Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Ku, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

APPLICANT: Steinmann, Kathleen

APPLICANT: FOR IDENTIFICATION, METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049
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2.0%; Score 74; DB 9; Length 1492;
Best Local Similarity 67.5%; Pred. No. 2.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Porter, Mark
APPLICANT: Donnan
APPLICANT: Donnan
APPLICANT: Donnan
APPLICANT: Johnson, Kory
APPLICANT: Gene Logic, Inc.
ITILE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
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                                                                                                            ; Sequence 1627, Application US/09917800A ; Patent No. US20020119462A1
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GENERAL INFORMATION:
APPLICANT: Oberley, Larry Wayne
APPLICANT: Oberley, Larry Wayne
APPLICANT: Smith, Benjamin Barnes
TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antis
TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antis
TITLE OF INVENTION: Oligonucleotides
TITLE OF INVENTION NUMBER: US/09/993,333
CURRENT APPLICATION NUMBER: US/09/993,333
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PASKSEQ for Windows Version 4.0
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Pred. No. 1.8e-11;
0; Mismatches 50; Indels
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Pred. No. 4.7e-11;
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PRIOR APPLICATION NUMBER: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13787
LENGIH: 2825
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Best Local Similarity 67.5
Matches 104; Conservative
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US-10-198-846-13787
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Best Local Similarity
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Search completed: April 1, 2004, 14:10:44 Job time : 1277.68 secs
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Best Local Similarity
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                            US-09-727-855B-6
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LENGTH: 597
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              APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialaguan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPRESENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 709, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA -0.028 US
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PELL PROGram
SSQ ID NO 709
LENGTH: 2208
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66.9%; Pred. No. 3.4e-10;
Live 0; Mismatches 50; Indels
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OTHER INFORMATION: Incyte ID No. US20020137081A1 241107.13
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bos taurus OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4
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Best Local Similarity 67.5%;
Matches 102; Conservative
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Matches 101; Conservative
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ORGANISM: Homo sapiens
PEATURE:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              JS-09-960-352-14744
                                                                                                                                                                                                                                              SEQ ID NO 14744
LENGTH: 424
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US-10-044-090-709
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GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: HOSHINO, Tatsuo
APPLICANT: OTHRA, KARUNA,
TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUI
FILLE OF INVENTION: PRATERIALS THEREOF
FILE REFERENCE: C38435/111694
CURRENT APPLICATION NUMBER: US/09/727,855B
CURRENT FILLING DATE: 2000-112-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN version 3.1
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Pred. No. 2.9e-10;
0; Mismatches 32; Indels
Sequence 6, Application US/09727855B Patent No. US20020168703A1
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l Similarity 73.6%;
89; Conservative
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ORGANISM: Phaffia rhodozyma
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GenCore version 5.1.6
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OM nucleic - nucleic	search, using sw model
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Title: US-09 Perfect score: 3632 Sequence: 1 tcc	US-09-727-855B-1 3632 1 tcctgttgataatctttctaaagagcttgaaccattgtag 3632
Scoring table: IDENTI Gapop	TY_NUC 10.0 , Gapext 1.0
Searched: 3470272	172 seqs, 21671516995 residues
Total number of hits	satisfying chosen parameters: 6940544
Minimum DB seq length: Maximum DB seq length:	h: 0 h: 200000000
Post-processing: Mini Maxi List	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		476	710	479	5713	4 Sequence 1	cDNA enco	AR222757 Segmence	58	≥		_	Macaca	Macaca	AB001693 Equus cab		1 '	BC010548 Mus muscu	BD190035 DNA array	E08013 DNA encodin	AY280719 Homo sapi		Ношо	AX526146 Sequence	Homo sapi	AROBES4 Synchelic	AR106627 Sequence	Sequenc	3			AX334340 Sequence	=	sequence	Kar mknA		AKU97395 Homo sapi		313 Sequenc	N O	7275 Pondo	0000	7291 (-) 131	a T
SUMMARIES 3 ID	1 1 1 1 1 1 1 1 1 1	34	BD01571	AX12847	BD01571	I6649	E15568	AR2227	ď	O MMNSO	0	ď	7				0	0 BC01054	BD190035		AY280719		AY280721		0	A		AR38080	HSMINSOD	AX75300	BC012423	AX33434	HSSOD	DATAMENT OF	>		AX 6 9 7 6 3						AB087	18
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ALIGNMENTS

RESULT 1

	T PAT 15-MAY-2001					rhodozyma	ricace I may		lobasidiales:				rly astaxanthin	
	linear					. Phaffia		mycetes;	Cvstofi				particulan	
	AX128476 3632 bp DNA		AX128476	AX128476.1 GI:14134943	•	Xanthophyllomyces dendrorhous (anamornh: Phaffia rhodozyma)	Xanthophyllomyces dendrorhous	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales:	Cystofilobasidiaceae; Xanthophyllomyces.		Hoshino, T., Ojima, K. and Setoguchi, Y.	Recombinant production of carotenoids, particularly astaxanthin	
AX128476	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	TITLE	

	Shàaagaacagaagctggtaagtcagtcagtcagtcagtcagt	CCCCCAGCCGAGGAAGAGCCGAGCCGCTCGTGAACGACAAA 9	WAGGCTTTCTCCATCTTAAGCTCATTCTCAACCGACTCATCTCGTTCCCAT 960	CATTCCCATCACTACGCCATCCATGTTCGAGATCCTTCCT	TTCGTCGCTCCTGCTTTCCACATCACGCCAAACATACCTCGCCTCGCTCG			1	261 GTCCTTGGTTTTTCTTGGCTTTGGTTGAAAATTCCTCTCCACTCAGGCCCTGGAGCCCTG 321 CATCTCCAAGGAGATCATGACCCTTCACCACAAGGACCATCAGACTTATGTTAAGGG				01 GGGAGATGAAGTTTGATGAGGGCTCATCGTCTAGCACGTTGACCGGATCT 01 GGGAGATGAAGTTTGATGAGGGGCTCATCGTCAGTGAGTG	61 CAAGTTCAACGGAGGAGGACACATCAATCGTCGGTGATATTCTTCAAACTCTTGGTGAG 21 AAGTCAGGTCAAGGTGACTGTTCGGCTTTCTGCGGGATCTATCT	21 A	
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JOURNAL Patent: EP 1111067-A 1 27-JUN-2001; F. HOFFMANN-IA ROCHE AG (CH) FEATURES Location/Qualifiers 1. 3632 /organism="Xanthophyllomyces dendrorhous" /do_trpe="unassigned DNA" /db_xref="taxon:5421" 5'UTR 922. 923	/note="EXPERIMENTAL" exon 986. i.096 intron 1097. i.306 exon 1307. i.1555 intron 1457. i.555	g g ;		INTron 24/32590 exon 23912507 polyA_site 26632664 /note="EXPERIMENTAL"	Onlein Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 3632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 TCCTGTTGATAATCTTTCTAACGCCTTGTACTTTGACCAAGGCGTTTGTCCGAAATTTTG 60	OY 61 CAAACTTAGTGTTGGTCGCATGGACGGTCTTCGGATCCAGAACTGACGGCTCGCCAATAA 120 	QY 121 AGTALGACGALGGERAGGAGGAACCACAGGTIGACCAGTCTCAAAGACTGCT 180 Db 121 AGTALGACGATGGTGAAGGAGAAACGAGAACCACAGGTTGACCAGTCTCAAAGAGTGCT 180	Qy 181 GATGEGGGAGGATTGFCATTAAATGGTGTTGTATATGCTAGAGCCAAGAGAACAT 240 	Qy 241 TTGGTTTTGGTTTTGCATTTGATGAGATGTGACGGTTGAAGAGGGGAGGAGG 300 	Qy 301 CTCACTAACCCAAGAAGCCAGGAGCAAGGAATGCCTCCCCTTTCATCAAGATCTTT 360 	Oy 361 CTCACATCGAACAITTGACAITCTCITIAGIAICCITICTATCTTTCTTCCAACTICTC 420	Qy 421 CCATTGTATCGACTTTGCTCGACTTGCTTTTTTTCTCTGAGAGAGA	Qy 481 ATATCGAAGGAGCACACACACATTGGAGTTAGGGTAACAGATGAAGAGGGCCCGAGGT 540 L	Qy 541 GGATGGGGCTGTAGGAAGTAGCTGATGAGTTCCTGGATGATGATGATGAGGCGAAGGAAC 600 1	601 AGACATAGGATCTCTGTCTCGTCCTGGAATTACTGAGTCTTGTATCCAGCGTGTT

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Qy 2821 GTTTATTATCTAATTCATGAACTATGGAACATATGGAATTTCCAGAACAA 2880 Db 2821 GTTTATTATCTAATTCATTGATTCATGCGACTATGGGATTTCCAGAACAA 2880 Qy 2881 ACAGATGCAACAAGCACGGCATTTTCCAAAGATCGAGTCCTCCCACAAGTATGCGGCAA 2940 Db 2881 ACAGATGCAACAAGCACGGCATTTTCCAAAGATCGAGTCCTCCCACAAGTATGCGGCAA 2940 C 2941 GGTTTGTTGTTAAAAAGCAGATTTTCCAAAGATCGAGAACAAATTTCCGAAGTTTTCCAAAGTATTCGACCTGTGC 3000 Db 2941 GGTTTGTTGTTAAAAAGAGATATAAAAAGCAGACAAAACAAATCGTTTATCGACCCTGTGC 3000 Db 2941 GGTTTGTTAAAAAGAGATATAAAAAACAGAACAAAACAA	QY 3001 ACCAACACCGTGACCGTTGACGACTTGGTAGTTGTTGCTGTTCAAAGGAC 3060 Db 3001 ACCAACACCGTGACCGTTTGACGACTTGGTAGATTGTTGTTGTTTCAAAGGAC 3060 QY 3061 TCCAACTTCCAAGCTTCAACAACTTCTCGGCACGTTCGTT	QY 3181 AGCTCAAGTCAACTCACATGTCTTTGGCGGTACCGAAGACGTTCTCAAGCTGCTTGG 3240 Db 3181 AGCTCAAGTCAACTCACATGTTTTGGCGGTACCGAAGACGTTCTCAAGCTGCTTGG 3240 QY 3241 AAGCTTTTCCGAGCTTGCCAGTAGGTCCCTGGTTGGAAGAAGTGTCGAAGGCTAAGG 3300 Db 3341 AAGCTTTTCCGAGCTTGCCAGTAGGTTCGAGAAGAATGTCGAAGATGTAGGGTAAGG 3300 QY 3301 GCGATGAAAAGCATGAGATATTAGCTATCGGCGCGATAAAAGTGTGCGAGATGAAAAT 3360 Db 3301 GCGATGAAAAGCATGAAGATATTAGCTATCGGCGCGATAAAAGTGTGACGAGATGAAAAT 3360	Oy 3361 GGAGAAAAGATGATTCGCACCATCGACCAACGACCAAGGAATGGAGGTGTCACCGGC 3420 Db 3361 GGAGAAAAAGATGATTCGCACCATCGACCACCAAAGGAATGGAGGTGTCACCGGC 3420 Qy 3421 CTTCCACTTCTTGTACTCCTCAACGTTGACGAAGGAATGGAGGTCGGTGGCCTTAGC 3480 Db 3421 CTTCCACTTCTTGTACTCCTCAACGTTGACGAAGATGACGAGCGTCGGTGGCCTTAGC 3480 Oy 3481 CTCCACTTCTTGTACTCCTCAACGTTGACGAAGAGAGAGA	QY 3541 ATGAGATGTCAGGATGCTTCACTGTAGATGGAGGAAGAATATGCGAAGGAAG	RESULT 2 BD015710 LOCUS BD015710 BD015710 BD015710 BD015710 BCCUS DEFINITION Recombination production of carotenoids, in particular, actaxanthin. ACCESSION BD015710 VERSION BD015710 VERSION BD015710 VERSION SD015710-10-11 GI:22556847 VEX.WORDS Anthophyllomyces dendrorhous Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetes; Heterobasidiomycetes; Tremellomyces. Cystofilobasidiaceae; Xanthophyllomyces. Cystofilobasidiaceae; Xanthophyllomyces. I (bases 1 to 3632) AUTHORS HOSHINO, T., Ojima, K. and Setoguchi, Y.
1681 GCATGATGAAACAGACTCTCTGTTCTGGAAGAACTTGGCTCCCTATGGATCCGAGGAGGC		ATGAT ATGAT TTCGT TTCGT TTCGT	CTTTCTTGAATAGTCGTAGCGTCTGATCTCGTTTTATTGACTGTTGTTGCTTCTGTCC 234 CTTTCTTGAATAGTCGTAGCGTCTGATCTCGTTTTATTGACTGAC	461 TTATCAACTACAAGGAGCCGAATTGCAGCTGCTCTCTAAGCGGGACGAAAG 252 461 TTATCAACTACAAGGAGCCCGATTGCAGCTGCTGCTCTTAAGCGGGACGAAAG 252 461 TTATCAACTACAAGAGGAGCCCCGATTGCAGGCTGCTCTCTAAGCGGGACGAAAG 252 521 TAACGACATATGAAGGAGCAATATCGTTTCTTCATAAACAACTTTCGAGGCAGAT 258 621 TAACGACATATGAAGGAGGATCAAATATCGTTTCTTCATAAACAACTTTCGAGGCAGAT 258 621 TAACGACATATGAAGGAGGATCAAATATCGTTTCTTCATAAACAACTTTCGAGGCAGAT 258	2581 GGGGGGTACTACAAGAGGTTTGTATGGAGAATTGAGTTTGTTCACGGTTAGCAGGT 2640 2581 GGGGAGGTACAAGAGGTTTGTATGGAGAATTGAGTTTGTTCACGGTTAGCAGGT 2640 2581 GGGGGGGTACGTACAAGAGGTTTGTTGAGGGTTAGCAGGT 2640 2641 TATGATATATGTAGCTATTGTCTCAAATTCTGAAGAAGAACAAGATGGTTTGTC 2700 2641 TATGATATATGTAGGCTATAGTCTAAATTCTGAAGAAGAACAAGATGGTTTGTC 2700 2701 GGAAGAGATTGAGGCTATAGTCTAATTCTGATGTCGAACAACATGCCCTGGTCTGC 2760 2701 CGAAGAGATTGAGAGCTCAGGTCATCTGATGTCGAACAACATGCCCTGGTCTGC 2760 2701 CGAAGAGATTGAGAGACCCGGTCATCTGATGTCGAACAACATGCCCTGGTCTGC 2760 2761 CAACAGTTTCTAGCACATTATGACCATGTTCATGTTGTAAATTGGGAAATGAGCCAGAAAAG 2820 2761 CAACAGTTTCTAGCACATTATGACCATGTTCATGTTGTAAATTGGGAAATGAGCCAGAAAG 2820 2761 CAACAGTTTCTAGCACATTATGACCATGTTCATGTTGTAAATTGGGAAATGAGCCAGAAAG 2820

421 CCNTTGTNTCGACTTTGCTCTTGTTATCTCTGAGNAGATGGGCATGCCA #66 491 ATATCGAGGGCGACACACACACACTTGGAGTTTGGGTAACACATGAGAGGGGCCGAGGT \$40 491 ATATCGAGGGCGACACACACACACTTGGAGTTTGGGTAACACATGAGAGGGGCCCGAGGT \$40 491 ATATCGAGGGCGCACACACACACTTGGAGTTTGGGGTAACATGAGAGGGGCCCGAGGT \$40 541 GAALCGAGGGCGACACACACACTTGGAGTTTGGGGTAACATTGAACACGCGAGGGCC 541 GAALCACACGGAACTCTGTGCTCTTGAATTGCTTGAGTTGATCACACACA	CCAGGAGATCATGACCCTTCACCACCAAGCACCATCAGACTTATGTTAACGG AGCTGCCGAGAAGAGAGCACCATCAGACTTATGTTAACGG ACGCTGCCGAGAAGAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGA
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TITLE Recombination production of carotenoids, in particular, astaxanthin JOURNAL, PRECEDUAL 2011, 17-JUL-2011, 18-JUL-2011, 18-JUL	241 TIGGITITICITITIGGITITICITITIGGITITICITITICITIC

3601 ATACACTTTGGAAAGAGCTTGAACCATTGTAG 3632	Qy 36 Db 36 RESULT 3 AX128479 LOCUS DEFINITION	ACGITTCTTCATAAACAACTTTCGAGGAGAI 258 ATCGTTTCTTCATAAACAACTTTCGAGGCAGAI 258 ATCGAGAAATTGAGTTTGACGGTTAGCAGGA 264 ATGGAGAATTGAGTTTGACGGTTAGCAGGT 264 ATGGAGAATTGATTGTTGACGGTTAGCAGGT 264	8 6 8
3541 ATGAGATGTCAGGATGCTTGCTTCACTGTAGATGGAGGAA(8 S	TTATCAACTACAAGGGGGGGGGGGGGGTTGGAGGGGGGGTGTCCGGGGGGGG	8 %
3481 CTCGGGCTCGTAGATGCTGATGAAACACAATAGGTAGTAGC 	ζς d	TTGGTCCG	oy Op
3421 CTTCCACTTCTTGTACTCCTCAACGTTGACGAAGATGACG 	රු සි	240	çç Dp
3361 GGAGAAAGGTGATTCGCACCATCGACGACCTCGACCAAA. 	č d	2281 CTTTCTTGAATAGTCGTAGCGTCTGATCTCGTTTTATTGACTGAC	දු දු
3301 GCGATGAAAGCATGAAGATATTAGCTATCGGCGCGTAA 	ò q	2221 TITICICGGGAIGAITICATAAACAGCTCACATICCTATCAGAGTIGACGTGCGTAT 2280 	දු පු
3241 AAGCTTTTCGAGCTTGCCAGTAGGTCCCTGGTTGGAGAA. 	QV DP	22 2	Qy Dp
3181 AGCTCAAGTCAACTCACATGTCTTTGGCGGTACCGAAGAC 3181 AGCTCAAGTCAACTCACATGTCTTTGGCGGTACCGAAGAC	<u>کې</u> م		ද්ර ප්
3121 AAAAGGCAAAAAGGAACAGAGCGATAAGCATATGTGATTC	& 9d	2041 CAAACTGACTATACATGTTTCTACAACAACAACAGGCTTGAACCGCTTACTAAGAAG 2100 	රු පු
3061 TCCAGACTGGACGCTTCCAAGCTTCAACAACTTCTCGGCA 	Qy Dp		Qy Dp
3001 ACCAACACCGTGACCGTTTGACGAGTTGGTAGAGTTGTAG 	Qy	198	λό qa
2941 GGTTTGTTGTTAAGAGATATAAAAGCAGACGACGACAAAACAA 	oy aga	3TCCTCTCCGGGGGTTCGACTGCACGTTCATAG 192 	Sy qa
2881 ACAGATGCAACAAGCACGGCATTTTCCAAAGATCGAGTC 2881 ACAGATGCAACAAAGCACGGCATTTTCCAAAGATCGAGTC	ço qa		QY DP
2821 GTTTATTATCTAATTCATTGATTCATGGGGCTATGGGATAC 2821 GTTTATTATCTAATTCATTGATTCATGGGACTATGGATAC	cy Dp	GGCTATCGAGGAATCTTTGGTTCTTTCGAGGG 180 	Qy Dp
2761 CAACAGITICIAGCACAITAIGACCAIGITCAIGIGIAAA 	Qy	TTTGGCTCCCTATGGATCCGAGGGGGC 174	85 AS
2701 CGAACAGATTGAGAGATCAAGCCCGGTCATCTGATGTCGA 	Qy Db	TIGITICIGCGGATCTATCTCATCTTGATTG 168	ζς Gg
2641 TATGATATGTAGCTATAGTCTAGTCTAAATCTGAAAGA 	QQ ab	1561 CAAGTICAACGGAGGAGACACATCAATCGTCAGTGATATTCTTCAAACTCTTGCTGAGC 1620 	ζζ G

GAAGAGAACAAGATGGTTTGTC 2700 GAACAACATGCCCTGGTCTGC 2760 TCCTCCCACAAGTATGCGGCAA 2940 AGTIGITGCTGTTCAAAGGAGC 3060 AAATCGTTTATCGACCCTGTGC 3000 PAGCGTCGCTGTTCGGGAAAAG 3120 CCTCTACTTCTTATAGGCTCTT 3180 AGTICICAAGCIGCTGCTTGG 3240 AGGAATGGAGGTGTCACCGGC 3420 AATTGGGAAATGAGCCAGAAAG 2820 ACATATGGGATTTCCAGAACAA 2880 AGGAATGGAGGTGTCACCGGC 3420 GAAGCAGTCGGTGGCCTTAGC 3480 GGAGAGAAAAGAGAAGATG 3540 AGAAGATATGCGAAGCAAGAC 3600

linear PAT 15-MAY-2001

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Gaps

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PAT 28-DEC-1997

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TCTAGCTCTTCTTCGTCCTTTCTGTCCTGCTCTTTGTTGATATTCAGCTCGATAGAC 1214
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(C12P23/00,C12R1:01),(C12P23/00,C12R1:18),(C12P23/00,C12R1:20),(C12P23/00,C12R1:465),(C12P23/00,C12R1:645),C12N15/00 CC
Recombination production of carotenoids, in particular, CC
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    .669 "Corganisms" Xanthophyllomyces dendrorhous" (mol_type="genomic DNA" /dol_xref="taxon:5421"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%; Score . 1.1e-13,
3.1%; Pred. No. 1.1e-13,
2.5; Mismatches 117;
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                                                                                                                                                                                                                                   Score 151.4; DB 6
Pred. No. 6.8e-31;
0; Mismatches 1
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                                                                        Location/Qualifiers
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Best Local Similarity 99.3
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                                                           astaxanthin
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KEIMTLHHTKHHQITVNGLKAAEESYSAAVGKEDVI.TQVKLGSALKTNGGGHINHSLF
KKINAPYGSEEATLSEGPLKKAIEESFGSFEAFKKFNADTAAVGGSGMGWLGINPLT
KKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARL
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Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
Xanthophyllomyces dendrorhous
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
Cystofilobasidiaceae; Xanthophyllomyces.
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PN JP 2001190294-A/4
PD 17-JUL-2001
PP 01-DEC-2000 JP 2000367089
PR 01-DEC-1999 EP 99123821.3
PI TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOGUCHI PC
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12P23/00, C12Q1/68// PC
                                                                                 Xanthophyllomyces dendrorhous
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
                                                                Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
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Recombination production of carotenoids, in particular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 669;
                                                                                                                                                                                                                                                                           /organism="Xanthophyllomyces dendrorhous"
/mol_type="unassigned DNA"
/mol_xref="taxon:5421"
1. .669
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99.3%; Pred. No. 6.8e-31;
ive 0; Mismatches 1;
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Hoshino,T., Ojima,K. and Setoguchi,Y.
Recombination production of carotenoids,
Patent: JP 2001190294-A 4 17-JUL-2001;
P. HOFFMANN LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATGTGCTTACCCAGGTTAAGCTTCAGTCTG 1457
                                                                                                                                     Cystofilobasidiaceae; Xanthophyllomyces.
                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AGGATGTGCTTACCCAGGTTAAGCTTCAGTCTG 262
                                                                                                                                                     1 Hoshino,T., Ojima,K. and Setoguchi,Y. Recombinant production of carotenoids, Patent: EP 1111067-A 4 27-JUN-2001; F. HOFFMANN-LA ROCHE AG (CH) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /protein id="CAC38928.1"
/db_xref="GI:14134947"
/db_xref="REMTREMBL:CAC38928"
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                             GI:14134946
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AX128479.1
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Seguence 5 from patent US 6432407.
AR222757
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/db_xref="taxon:37769"
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/product="MnSOD"
                                                       GI:23330439
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                                                       AR222757.1
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        1215 TAACCCATCTCATCTCCTGGACATTCTTTTACTGGAAACGTATCTTGTCCTTGGTTTTTC 1274
                       PAT 28-JUL-1999
                                                                                                                                                                                                                                                                                1 (bases 1 to 728)
Takesako, K., Daimon, H., Kuroda, M., Katou, I., Yasueda, H., Akiyama, K.
and Yamaguchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                   KATOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1365 AGACTTATGTTAACGGCCTCAACGCTGCCGAGGAGGCTACTCGGCCGCTGTGGGCAAGG 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide 1. .618 //product='Malassezia antigen protien MF-3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              PI YASUEDA HIROSHI, AKIYAMA KAZUO, YANAGUCHI HIDEYO PC
CO7K14/195, A61K39/35, CO7H21/04, CO7K7/08, C12N15/09, C12Q1/68, PC
G01N33/53,
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JP 1998077296-A/3
24-MR-1998
05-SEP-1996 JP 1996257613
TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                          RECOMBINÂNT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
Patent: JP 1998077296-A 3 24-MAR-1998;
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                                                                                                                                                                    linear
                                                                                                                                                              728 bp DNA line
cDNA encoding Malassezia antigen protein MF-3.
E15568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                               1275 ITGGCTTTGGTTGAAATTCCTCT 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                       JP 1998077296-A/3. unidentified
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                                                                                                                                                                                                                                                       unidentified
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Heterobasidiomycetes, Tremellomycetidae, Tremellales, Tremellaceae,
Filobasidiella.
                                                                                                                                 Unclassified.

Unclassified.

(Conclassified.)

Takesako,K., Okado,T., Yagihara,T., Kuroda,M., Onishi,Y., Kato,I., Akiyama,K., Vasueda,H. and Yamaguchi,H.

Antigenic protein originating im malassezia

Patent: US 6432407-A 5 13-AUG-2002;

Location/Qualifiers

1. 728
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Narasipura S.D., Chaturvedi, V. and Chaturvedi, S.
Direct Submission
Submitted (128-SEP-2003) Mycology, Wadsworth Center, 120 New Scotland Ave, Albany, NY 12208, USA
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Cryptococcus bacillisporus
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Cryptococcus bacillisporus MnSOD mRNA, complete cds.
AY423629
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linear
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Narasipura, S.D., Chaturvedi, V. and Chaturvedi, S.
Complete cDNA of MnSOD of Cryptococcus neoformans
Unpublished
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mRNA
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Mus musculus (house mouse)
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729^730
/citation=[1]
/replace="g"
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ilarity 69.5%;
Conservative
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Best Local Similarity 69.5
Matches 107; Conservative
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                                                                          Query Match
Best Local Similarity
Matches 107; Conserv
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X04972.1
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                                                                                                            2389 AGATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGACTATCTCGCTG 2448
                                                                                                                                                                                                                                                                               ROD 17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 779)
Hallewell, R.A., Wullenbach, G.T., Stempien, M.M. and Bell, G.I. Sequence of a ODNA coding for mouse manganese superoxide dismutase Nucleic Acids Res. 14 (23), 9539 (1986)
                                                                                                                                          560 ACATCTGGGAGCATGCTTTCTACCTTCAGTACAAGAACGTCAAGAGCCCGATTACCTCAACG 619
                                                                                                                                                                                                     ccarcriggeacerrarcaacracgaggaggccgagaaccgrcrgaaggcrgcccrgrga 678
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Sequence of manganese superoxide dismutase-encoding cDNAs from
                                                                                                                                                                        CTGTTTGGTCCGTTATCAACTACAAGGAGGCAGGCCCGATTGCAGGCTGCTCTTAA
                                                                               Gaps
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/strain="BALB/c and/or C3H"
/db_xref="taxon:10090"
/fissue type="liver, kidney, brain, spleen, heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-NOV-1992) Sun Y., FCRDC, CBS, LVC, P.O. Box
Frederick, MD, 21702-1201
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                                                                                                                                                                                                                                                                              MANSODRX 179 bp mRNA linear M.musculus mRNA for manganese superoxide dismutase.
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/product="manganses superoxide dismutase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // 6. .704
/ codon start=1
/product==manganese superoxide dismutase"
/protoin_id==CAA/9308.1"
/db_xref=="G1:288505"
/db_xref=="G0A:P09671"
/db_xref==G0A:P09671"
                                                                               23; Indels
                                                 Length
                                                 Score 82.2; DB 8;
Pred. No. 2.6e-11;
                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                            dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Gene 131 (2), 301-302 (1993)
                                                                                                                                                                                                                                                                                                                          Z18857.1 GI:288504
manganese superoxide dismu
Mus musculus (house mouse)
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/citation=[1]
/replace="tg"
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/replace="a"
                                                 2.3%;
llarity 80.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 779)
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les 96; Conser'
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OIMOLHHSKHHAAVUNNINATEEKYHEALAKGDVTTQVALQPALKFNGGGHINHTIFW
TNLSPKGGGBPKGELLEAIKRDFGSFEKFKEKLTAMSVGVQGSGWGWLGFNKEQGRLQ
IAACSNQDPLGGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYT
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/translation="MLCRAACSTGRRLGPVAVAAGSRHKHSLPDLPYDYGALEPHINA
                                                                                           1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCACCAAGCACCATCAG 1366
                                                                                                                                                                                            1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 897)
Hallewell,R.A., Mullenbach,G.T., Stempien,M.M. and Bell,G.I.
Sequence of a CDNA coding for mouse manganese superoxide dismutase
Nucleic Acids Res. 14 (23), 9539 (1986)
37997253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROD 18-MAY-1994
                                                                                                                                 204 GCCTACGTGAACAACCTCAACGCCACGAGGAGAAGTACCACGAGGCTCTGGCCAAGGGA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 GCGCTGGAGCCACACTTAACGCGCAGATCATGCAGCTGCACCACCAGCAGCACCATGCG
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Length 779;
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/protein_id="CA#28645.1"
/db_xref="GI:53450"
/db_xref="GOA:P09671"
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125. .718
/product="manganese superoxide dismutase"
897.
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Pred. No. 2.5e-10;
                                                47;
     DB 10;
                                                                                                                                                                                                                                                                                                 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                          GATGITACAACTCAGGTCGCTCTTCAGCCTGCAC 297
Score 78.8; DB 10
Pred. No. 2.4e-10;
0; Mismatches 47
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/db_xref="taxon:10090"
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DEFINITION

COCUS

RESULT 11 AB087277

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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

REFERENCE AUTHORS

JOURNAL

TITLE JOURNAL

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Direct Submission
Submission
Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
Kyoto University, Center for Human Evolution Modeling Research;
Kanrin, Innyama, Aichi 484-8506, Japan
(E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNYTEE
KYSPALAKOPVTAQLPALOPALEHGGGALINHSI PWTWLSPNGGGEPKGELLEAIKRDF
GSFEKEKEKLTAASVGVGGSGWGWLGPNKERGQLQIPECPNQDPLQGTTGLIPLLGID
VWEHAYYLQYKNVRPDYLKAIWNVINWENYTERYMACKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                             Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate
superoxide dismutases
Gene 296, 99-109 (2002)
2 (Dases 1 to 600)
Fukuhara,R. and Kageyama,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GCCTGGAGCCTCACATCAACGCGCAGATCATGCAGCTGCACCACACCAGCACCACGCG
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Macaca mulatta mRNA for Mn-superoxide dismutase, complete cds.
AB087279
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|roduct==mh-euperoxide dismutase"
|protein_id="BAC20357.1"
|db_xref="GI:23503534"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
1. .600
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                       Mammalia, Eutheria, Primates;
Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                     Fax:81-568-63-0085)
Location/Qualifiers
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2 (bases 1 to 600)
Fukuhara,R. and Kageyama,T.
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AB087279
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KYGBALAKRODYTAQIALQPALKENGGGHINHGIPWTNLSPNGGGEPKGELLBAIKRDF
GSFEKEKEKLTAASVOVQGSGWGWLGFNKERGQLQIAACPNQDPLQGTTGLIPLLGID
VWEHAYYLQYKNVRPDYLKAIWNVINWRNYTERYMACKK"
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                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate superoxide dismutases
Gene 296, 99-109 (2002)
2 (bases 1 to 600)
Fukuhara,R., and Kageyama,T.
                                                                                                                                                                                       AB087277 600 bp mRNA linear PRI 04-OCT
Macaca fuscata mRNA for Mn-superoxide dismutase, complete cds.
AB087277
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/product="Mn-superoxide_dismutase"
/protein_id="BAC20356.1"
/db_xref="GI:2359528"
          GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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                                                          281 GATGTTACAACTCAGGTCGCTCTTCAGCCTGCAC 314
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Macaca fascicularis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Macaca fuscata"
                                                                                                                                                                                                                                                                                                                  Macaca fuscata (Japanese macaque)
Macaca fuscata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9542"
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                     AB087277.1 GI:23503531
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AB087278.1 GI:23503533
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          1427
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Best Local 8
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CDS

FEATURES

LOCUS DEFINITION ACCESSION VERSION

RESULT 12 AB087278

ORGANISM

KEYWORDS SOURCE

Matches

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ORIGIN

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/tränslation="wkhsledlpdlpydygalebhinaoimolhhskhhaayvnnlnvyee
kyoralakkopytaoialopalkenggchinhsifwtnlspngggepkgelleaikkdf
gsfdkfkekltatsvgvggsgwgwlgfnkerghloiaacpnodplogtyglifligid
vwehayyloyknvrppylkaiwnvinwenvterymackk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 296, 99-109 (2002)
2 (Dases I to 600)
Pukuhara,R. and Kageyama,T.
Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute, Kyoto University, Center for Human Evolution Modeling Research; Kanrin, Innyama, Aichi 484-8506, Japan (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
                                                                             /product="manganese superoxide dismutase"
/protein id="BAA76922.1"
/b.xref="dl="BAA76922.1"
/b.xref="dl="MLCRAACSTSRKLVPALGSLGSRQKHSLPDLQYDYGALEPYINA /translation="MLCRAACSTSRKLVPALGSLGSRQKHSLPDLQYDYGALEPYINA QIMQLHHSKHHAAYYNNLNYTERYQBALAKGDVTAQIALQFAKRNGGAINHTIFW TNLSPNGGGEPKGKLLDAIKRDFGSFDKFKEKLTAVSAGVGSGWGWLGFNKDQGRLQ TNLSPNGDPLGGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVSERYM ACKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1367 ACTIAIGITAACGGCCTCAACGCTGCCGAGGAGAGAGTACTCGGCCGCTGTGGGGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 gėcitatiensaacadongaacingaacingas paradis paradia paradia paradis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure, molecular evolution, and gene expression of primate superoxide dismutases
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Hylobates lar mRNA for Mn-superoxide dismutase, complete cds.
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                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 77.2; DB 4; Length 954; 68.8%; Pred. No. 7.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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/product==mn-superoxide dismutase"
/proein_id="BAC20355.1"
/db_xref="GI:23503530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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ilarity 68.2%; Pred. No. 1.9e-09;
Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hylobates lar"
/mol_type="mRNA"
/db_rref="taxon:9580"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
70. .738
/gene="Mn-SOD"
/codon_start=1
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AB087276.1 GI:23503529
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Best Local Similarity
Matches 105; Conserv
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Matches 106;
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TITLE
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VERSION
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JOURNAL
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  CDS
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                                                                                                                                                                                                                                                                                                                     /translation="MKHSLPDLPYDYCALEPHINAQIMQLHHSKHHAAYVNNLNVTEE
KYQEALAKGDYTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGEPKGELLEAIKRDF
GSFEKFKEKLTAASYGVQGSGWGWLGFNKERGQLQIAACPNQDPLQGTTGLIPLLGID
VWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK"
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The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD
and Mn-SOD, and these expressions in equine tissues
J. Vet. Med. Sci. 61 (3), 291-294 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-MAR-1997) Nobushige Ishida, JRA Equine Research
Institute, Laboratory of Molecular and Cellular Biology; 321-4,
Tokami-Cho, Utsunomiya, Tochigi 320-0856, Japan
(B-mail:noishida@center.equinst.go.jp, Tel:81-28-647-0662,
Fax:81-28-647-0686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Indels
                                                                                                                                                                                                                                        /product="Mn-superoxide dismutase"
/protein_id="BAC20358.1"
/db_xref="G1:23503536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 77.2; DB 9;
Pred. No. 6.6e-10;
0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB001693.1 GI:4589877
Mn-SOD; manganese superoxide dismutase.
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/mol_type="mRNA"
/strain="Thoroughbred"
                                                                                               organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/note="domestic horse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    954 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equus caballus Mn-SOD mRNA for complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db xref="taxon:9796"
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                Location/Qualifiers
1. .600
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                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 954)
[shida, N.
                 Fax:81-568-63-0085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB001693
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Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
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Roe, B.A. and Murphy, J.W.
Comparison of highly conserved intronic and exonic elements associated with splicing among five diverse fungal organisms Unpublished (2003)
Other ESTS: jskorj2.rl
Contact: Murphy, JW
Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
Oklahoma City, OK 73190, USA
Tel: 405-271-2133 exz133
Email: juneann-murph@ouhse.edu
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This clone is available from the Fungal Genetics Stock Center,
Phone 913-588-7044, http://www.fgsc.net/ Contact Dr. Bruce Roe
Lobce@ou.edu, www.genome.ou.edu) for sequencing questions Contact
Dr. Juneann Murphy(juneann-murphy@ouhsc.edu) for library
      This clone is available from the Fungal Genetics Stock Center, Phone 913-588-7044, http://www.fgsc.net/ Contact Dr. Bruce Roe (broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact Dr. Juneann Murphy(juneann-murphy@ouhsc.edu) for library information.
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/clone="13g17j2"
/lab host="E. coli strain SOLR"
/clone lib="Cryptococcus neoformans strain B3501"
/note="Vector: pBluescript sk-; Site_1: EcoRI at 5'
cDNA insert; Site_2: XhoI at 3' end of cDNA insert"
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Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
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Dr. Juneann Murphy(juneann-murphy@ouhsc.edu) for library
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KUPFET, D.M., Drabenstot, S.D., Buchanan, K.L., Lai, H., Dyer, D.W.,
Roe, B.A. and Murphy, J.W.
Roe, B.A. and Murphy, J.W.
Comparison of highly conserved intronic and exonic elements
associated with splicing among five diverse fungal organisms
L Unpublished (2003)
Other_ESTS: 13917j2.r1
Contact: Murphy, JW
Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
Oklahoma City, OK 73130, USA
Tel: 405-271-2133 ex2133
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neoformans var. neoformans cDNA clone 13g17j2 3', mRNA sequence.
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cDNA insert; Site_2: XhoI at 3' end of cDNA insert"
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cDNA insert; Site_2: XhoI at 3' end of cDNA insert"
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Nikaido, I., Osaco, N., Satcukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osaco, N., Satto, R., Suzuki, H., Yamanaka, I., Styosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, K., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, D.M., Kanapin, A., Matsuda, H., Ercher, C.F., Forrest, A., Erzer, K.S., Gaasterland, T., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fleccher, C.F., Forrest, A., Fazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kawaji, H., Kawasawa, Y., Rezer, K.S., Gasterland, T., Kawasawa, Y., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, D., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Sandslin, J.V., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sandelin, A., Schneider, C., Reed, D.J., Reid, J., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watcanbe, Y., Wallining, L.G., Whinhaw-Boris, A., Yanagisawa, M., Yang, I., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakauuran, N., Sato, K., Shiraki, T., Konaka, J., Aizawa, K., Sthiraki, T., Washau, J., Aizawa, K., Sthiraki, T., Washau, J., Aizawa, Y., Itoh, M., Kagawa, T., Miyazaki, T., Sakai, K., Sakai, D., Shibata, K., Shinagawa, M., Washaulan, R., Rogers, J., Birney, B. and Hayashizaki, Y., Sakai, K., Sakai, D., Shibata, K., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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                                                                                                                         2448
                                                                                                                                                                                                                         2449 CTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCGATTGCAGGCTGCTCTAAG 2508
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BY327888 RIKEN full-length enriched, synovial fibroblasts Musmussculus CDNA clone L030044H15 5', mRNA sequence.
                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                81
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 337)
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He Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                        2389 AGAICIGGGAGCACGCTITCTACCTICAGTACAAGAACGICAAGCCTGACTAICTCGCTG
                                                                                                                                                                200 ACATOTIGGGAGCACCTITOTATOTICCAGTACAAGACGTCAAGCCCGACTATOTICAATG
                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
                                                              .,
  DB 14; Length 400; 1e-08;
                                                           30; Indels
                                                        0; Mismatches
  Score 85;
Pred. No.
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2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                  CTTTATGAACAAT 68
                                                  Matches 103; Conservative
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                          Local Similarity
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Query Match
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COMMENT
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BY327888
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KEYWORDS
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SOURCE

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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sarci, Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mam. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Exploration Research Group in Riken cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Prepare mouse tissues.

Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Releming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 dcdctdcacacatarraacgcdcadarcardcacgctgcactdcacacadaacacatacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1427 GATGIGCTTACCCAGGITAAGCTTCAGTCTGTAC 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/db_xref="taxon:10090"
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ORIGIN

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Carticold. S. Belbelling. Comming S. Dallals. Program: T. A. Carticold. S. Carticold.
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FEATURES

JOURNAL MEDLINE PUBMED

COMMENT

TITLE

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/clone_lib="Melcon Mouse R16 5 Pancreas Library 2 M16B2" /note="Organ: Pancreas; Vector: pBluescript II SK; Site_1: Mot!; Site_2: Sall; Library constructed using Superscript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming-Size-selected by column fractionation; average insert size 1.06kb. Primary library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ086753 359 bp mRNA linear EST 05-APR-2002 ih89d09.yl Melton Mouse E16 5 Pancreas Library 2 M16B2 Mus musculus cDNA clone IMAGE:5939369 5' similar to SW:SODM MOUSE P09671 SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECUESOR; ", mRNA
                                                                                                                                                                                                                      1367 ACTIATGITAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGGCAAGGAG 1426
                                                                                                        1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAG 1366
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center This clone is
available royalty-free through LINL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTS: ih89409.x1
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
                                                         0
  Length 353;
                                                         Indels
Score 78.8; DB 13;
Pred. No. 2.8e-07;
0; Mismatches 47;
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/dev stage="Embryonic day 16.5"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                         1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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/clone="IMAGE:5939369"
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/strain="ICR"
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     2.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 617-495-1812
              Query Match
Best Local Similarity 69.5'
Matches 107; Conservative
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JOURNAL
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AUTHORS
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BQ086753
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mussali, Caradaki, C. I (Dasca), M. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yananaka, T., Kiyosawa, H., Yananaka, T., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Bataloch, C., Golobori, T., Schriml, L. M., Kanaphin, A., Matsuda, H., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gastelnidi, M., Hirokawa, N., Jackson, I.J., Javvis, E.D., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Mattais, L., Marchionni, L., Morkenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pallai, K., Pontius, J.U., Miki, H., Nagashima, T., Petrovsky, N., Pallai, K., Pontius, J.U., Miki, H., Nagashima, T., Read, J.C., Reed, D.J., Reid, J., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M., Shimada, K., Sullana, R., Takenaka, Y., Taylor, M., Stanapisawa, M., Sanosi, L., Wanger, L., Wanger, L., Wanger, L., Wanger, L., Wanger, L., Wanger, C., Semple, C.A., Setou, M., Shimada, K., Yang, I., Yang, I.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNas
Nature 420, 563-573 (2002)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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                                                                           Score 78.8; DB 13;
Pred. No. 2.8e-07;
0; Mismatches 47;
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Best Local Similarity 69.5%;
Matches 107; Conservative
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sequencing profile with 384 multicapillary sequencer. Genome Res. 10 (11), 175-171 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genome Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.

Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Alzawa, K., Kimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T. Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Ohno, M., Sakai, K., Sakaume, M., Sakai, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Shiraki, T. Tagami, M. Waki, K., Watahiki, A., Muramatsu, M. and Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system--384-format
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2.2%; Score 78.8; DB 13; Length 359;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1420017L02"
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URL:http://genome.gescrriken.go.jp,
URL:http://genome.gescrriken.go.jp,
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genes. Genome.Res. 10 (10), 1617-1630 (2000)
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Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Tel: 81-45-503-9222
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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/clone lib="RIKEN full-length enriched, B16 F10Y cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="G370031F20"
                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BY310981.1 GI:26501318
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="stroma cell"
/clone_lib="RIKEN full-length enriched, stroma cell"
                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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BX300950 RIKEN full-length enriched, 14.5 days embryo RP+/+
Rathke's pouches Mus musculus cDNA clone K720012M21 5', mRNA
                                                                                                                                                                                                                                                                                                                                         DB 13; Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Score 78.8;
Pred. No. 2.8
                                                                                   organism="Mus musculus"
                                                                                                                                                                 /db_xref="taxon:10090"
/clone="1320017112"
                            Socation/Qualifiers
                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
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further details
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VERSION
KEYWORDS
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                          FEATURES
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Email: genome-resegsc.riken.go.jp,

WRL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Itoh,M., Kawai,J., Konno,H.,
Hivozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,T., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 675-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res .10 (10), 1617-1630 (2000)
                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1367 ACTIATGITAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library, Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GCCTACGTGAACAACCTCAACGCCACCGAGGAGGAGGTACCACGAGGCTCTGGCCAAGGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing pipeline with 384 muiticapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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_clone_lib="RIKEN full-length enriched, 14.5 days embryo
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Tissues were provided by Michelle Brinkmeier and Sally Camper (Bobt. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI 48109-0638 USA) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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69.5%; Pred. No. 2.8e-07;
tive 0; Mismatches 47
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/db_xref="taxon:10090"
/clone="K720012M21"
Contact: Yoshihide Hayashizaki
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CA889637
B0154B09-SN NIA Mouse Neural Stem Cell (Differentiated) CDNA
Library (Long) Mus musculus CDNA clone NIA:B0154B09 IMAGE:30098996
S,, mRNA sequence.
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Piao,Y., Dudekula,D.B., Qian,Y., Martin,P.R., Aiba,K., Vescovi,A.L. systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
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0273-74 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mann sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mus. 1 (bases 1 to 511)
Mux., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S. W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H. Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse_E14.5 retina lambda ZAP II Library"
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Contact: Klein WH
Contact: Klein WH
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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Pred. No. 2.8e-07;
0; Mismatches 47;
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240 GATGTTACAACTCAGGTCGCTCTTCAGCCTGCAC 273
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Matches 107; Conservative
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/tissue_type="round spermatids, pooled from multiple mice"
/dev stage="60 day"
/lab host="DH10B (phage-resistant)"
/clone_ilb="McCarrey Bddy round spermatid"
/clone_ib="mcCarrey Bddy round spermatid"
/note="Organ: testis; Vector: pBluescript SK+
/note="Organ: pBluescript Sk+
/note="Organ: testis; Vector: pBluescript Sk+
/note="Or
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata, Crinidae; Muridae; Muridae; Musnae; Mus.

1 (Dases 1 to 407)
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M., Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S., Bennett, J., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics) - excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences).

MGI:2072729
Seq primer: Primer name ambiguous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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         DISMUTASE [MN], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
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/mol_type="mRNA"
/strain="CD-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                          Mus musculus (house mouse)
                                                           CB274248
CB274248.1 GI:28464571
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/note="Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Five libraries representing E10.571.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library DNA was normalized by method #4 from Bonaldo, Lennon, and Scares 1996 Genome Research 6:791-806; O.5 microgram single-stranded mixed library plasmid DNA was nicrogram single-stranded mixed library plasmid DNA was single-stranded mixed library plasmid mixed library lib
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1947051 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                          Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tasgareishvili,R., Budocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ic86907.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Both for embryonic & newborn, male for adult and adult islet"
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/clone lib="Melton Normalized Mixed Mouse Pancreas 1
N1-MMSI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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'clone="IMAGE:5660725"
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Mus musculus
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/strain="ICR"
               GI:15689003
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insert size is about
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 écectégadechendatrandecedadricarechechechechedadechechique 262
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                                                                                                National Institute on Aging/National Institutes of Health 313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgun.grc.nia.nih.gov Plate: B0154 row: B column: 09 Seq primer: -21M13 Reverse High quality sequence stop: 566 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2%; Score 78.8; DB 14; Length 566; 69.5%; Pred. No. 2.8e-07; ive 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="niaEST:B0154B09-5N"
|db_xref="taxon:10090"
|clone="NIA:B0154B09 IMAGE:30098996"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dev stage="Adult"
|ab_host="DH10B"
                                                                     Contact: Dawood B. Dudekula
CDNA Library (Long)
                                          Unpublished (2002)
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BI713308
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Query Match Best Local

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DEFINITION RESULT 14 BI713308 LOCUS

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Library constructed and donated by J. McCarrey, Ph.D.
Gouthwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
                                                                                                                                                                                                                                                                                                                                                                                                                                       BU741935
mai50e03.yl McCarrey Eddy round spermatid Mus musculus cDNA clone
IMAGE:6449477 5' similar to SW:SODM MOUSE P09671 SUPEROXIDE
DISMITASE [MN], MITOCHONDRIAL PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus

Mus musculus

Mus pulazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 589)

Mocarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M., Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S., NIEHS Mouse

Unpublished (2002)
170 GCCTACGTGAACAACCTCAACGCCACCGAGGAGAAGTACCACGGGGGTCTGGCCAAGGGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single-stranded phagemids were prepped and tranformed into DH10B. Library contains 98.5% recombinants. References: J. Androl. 20:635-639 and Gene 25:263-269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Health Sciences). Original lambda-base
available through ATCC, catalog #63423.
                                                                                                                                                1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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High quality sequence stop: 428.
Location/Qualifiers
1. .589
/ organism="Mus musculus"
/mol type="mRNA"
/strain="CD-1"
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/clone="IMAGE:6449477"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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BU743935.1 GI:23692080
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Fax: 314 286 1810
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VERSION
KEYWORDS
SOURCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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BU743935
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0; Gaps

Length 589; Indels 0

Query Match 2.2%; Score 78.8; DB 13; Best Local Similarity 69.5%; Pred. No. 2.8e-07; Matches 107; Conservative 0; Mismatches 47;

Search completed: April 1, 2004, 21:52:24 Job time : 9345 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

April 1, 2004, 10:57:14; Search time 255.87 Seconds (without alignments) 7877.372 Million cell updates/sec

US-09-727-855B-1 3632

1 tootgttgataatotttota.....aagagottgaaccattgtag 3632 Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

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1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

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Issued Patents NA:*

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(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 98 7 6 12	44.27	000000 000000	829 1032 594 681 969	40000	US-09-023-655-1348 US-09-075-019-1 US-09-075-019-1 US-08-556-486A-27	134
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Length 7218;

DB 1;

2.6%; Score 94.8;

Query Match

Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Patent No. 5240847 Sequence 34, Appl Sequence 39, Appl Sequence 33, Appl Sequence 2, Appli Sequence 2, Appli Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 6324, Appl Sequence 8224, Appl Sequence 8224, Appl Sequence 8224, Appl Sequence 8224, Appl Sequence 8224, Appl Sequence 13, Appl Sequence 13, Appl		
28 58 1.6 495 1 US-08-133-711-41 29 57.6 1.6 491 1 US-08-133-711-42 30 56.8 1.6 521 4 US-08-133-711-42 31 55.8 1.5 522 6 5240847-5 33 51.2 1.4 491 1 US-08-133-711-38 35 50.6 1.4 491 1 US-08-133-711-38 36 49.8 1.4 4411529 3 US-09-103-840A-1 38 49.8 1.3 490765 3 US-09-103-840A-1 39 49 1.3 491 1 US-08-133-711-33 40 48.8 1.3 490 1 US-08-133-711-43 40 48.8 1.3 64 4 US-09-252-991A-7972 41 48.8 1.3 705 4 US-09-252-991A-7972 42 48.8 1.3 705 4 US-09-252-991A-7972 43 47.6 1.3 427 4 US-09-103-4140	ALIGNMENTS	RESULT 1 US-08-222-463-14 US-08-222-463-14 US-08-222-463-14 US-08-222-463-14 Sequence 14, Application US/0822463 Patent No. 5570367 GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Folgy & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA CONTURY: USA CONTURY: USA CONTURY: BADABLE FORM: MEDIUM TYPE: Floppy disk CONTURY: BADABLE FORM: MEDIUM TYPE: Floppy disk CONTURY: BADABLE FORM: MEDIUM TYPE: Floppy disk CONTURY: AS: POSSIBLE OF CONTURY: USA SOFTWARE: PAPLICATION DATA: CONTURY: ADPLICATION NUMBER: US/08/232,463 FILING DATE: APPLICATION NUMBER: BP 31 114 300.6 FILING DATE: 26-A10-1991 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 29,768 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. TELEFONMINICATION INFORMATION: TELEFONMINICATION: TELEFONMINICATIO

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SEQUENCE CHARACTERISTICS
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         Best Local Similarity 3.1%; Pred. No. 3.3e-18;
Matches 12; Conservative 255; Mismatches 117; Indels
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TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
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COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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US-09-091-097-5
'Sequence 5, Application US/09091097
'Patent No. 6432407
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NAME: WEINER: 3.181
REGISTRATION NUMBER: 32.181
REFERENCE/DOCKET NUMBER: 1422
TELEPHONE: 703.205.8000
TELEPHONE: 703.205.8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKADO, TAKASHI
YAGIHARA, TOMOKO
KURODA, MASANOBU
ONISHI, YOSHIMI
KATO, IKUNOSHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAKESAKO, KAZUTOH
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YASUEDA, HIROSHI
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APPLICANT: TAKESA
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APPLICANT:
APPLICANT:
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APPLICANT:
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Patent No. 5985633;
GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 728;
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APPLICATION NUMBER: US/08/977 7777 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.3%; Score 84.2; DB 4;
Best Local Similarity 71.9%; Pred. No. 1.2e-15;
Matches 110; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425 AGGATGTGCTTACCCAGGTTAAGCTTCAGTCTG 1457
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CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD,
STREET: 28 State Street, Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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TYPE: nucleic acid
STRANDEDNESS: single
LENGTH: 728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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USA
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1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGGCTACTCGGCCGCTGTGGGCAAGGAG 1426
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Jeffrey J. Seilaner
APPLICANT: Jeffrey J. Seilaner
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                         151 GCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTGCACCACCACGCAGCACCACGCG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/023,655
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                                                                                                                                                                                                                                                     271 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 304
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67.5%; Pred. No. 2e-12;
ttive 0; Mismatches 5:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REBERENCE/POCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                   RESULT 5
18-09-023-655-1348
'S equence 1348, Application US/09023655
'Patent No. 6607879
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Best Local Similarity 67.59
Matches 104; Conservative
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CALIFORNIA
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US-09~023-655-1348
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                                                                                                                                         Gaps
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GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVUE & COCKFIELD
STREET: 28 State Street, Floor 24
                                                                                                                                         0:
                                                                                       Query Match 2.0%; Score 74; DB 2; Length 813; Best Local Similarity 67.5%; Pred. No. 2e-12; Matches 104; Conservative 0; Mismatches 50; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,052
FILING DATE:
CLASSIPICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bub PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/927,230
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-151-052-1; Sequence 1, Application US/09151052; Patent No. 6107070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAWE: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
mat_peptide
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STATE: Massachusetts
COUNTRY: USA
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                         ; LOCATION:
US-08-927-230A-1
    NAME/KEY:
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1367 ACTIATGITAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426

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Length 594; Indels

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1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAG 1366
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; Patent No. 619058
; GENERAL INPORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
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APPLICATION NUMBER: US/09/075 ***

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   2.0%; Score 72.4; DB 3;
66.9%; Pred. No. 4.9e-12;
tive 0; Mismatches 51;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Kovarik, Joseph E.
REGIESTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 681 base pairs
TYPE: nucleic acid
                                   LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                          1..594
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Best Local Similarity
Matches 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Denver STATE: CO
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                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                          LOCATION:
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   235 GCCTACGTGAACAACCTGAAÓGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 294
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TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                         5240847-25
;Patent No. 5240847
; APPLICANT: HECKL, KONRAD;SPEVAK, WALTER;OSTERMANN, ELINBORG;
;ZOPHEL, ANDREAS;KRYSTEK, EDELTRAUD;MANRER-FOGY, INGRID;
;YOPHEL, ANDREAS;KRYSTEK, EDELTRAUD;MANRA, CHRISTIAN;HAUPTWANN, RUDOLF
;WICHE-CASTANON, MARIA J.;STRATOWA, CHRISTIAN;HAUPTWANN, RUDOLF
ITILE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; Score 74; DB 6; Length 1032; 67.5%; Pred. No. 2.4e-12; tive 0; Mismatches 50; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CAPRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
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                                                                              1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
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                                                                                                                                              295 darctracacccadaraccrcrrcacccrccac 328
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STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
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NAME: KOVATIK, JOSEPH E.
REGISTATION NUMBER: 33,005
REFERENCE, DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEFAN: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
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LENGTH: 1032
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Best Local Simi:
Matches 104;
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STATE: CC
COUNTRY:
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Length 681;

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1367 ACTIATGTIAACGGCCTCAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGGGCAAGGAG 1426
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MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION SI4
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/08/86,486
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-194
APPLICATION NUMBER: 38,615
RICHARD SHOLE APPLICATION NUMBER: 38,615
REPERENCE/DOCKET NUMBER: 324-0960
INPORMATION POR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
ITELEPANE: INCLEA
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Pred. No. 7.2e-12;
0; Mismatches 51;
                                                                                                                                                                   289 GAIGITACAGCCCAGATAGCTCTTCAGCCTGCAC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08880342
Patent No. 6218179
                                                                                                                         1427 GAIGIGCITACCCAGGITAAGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.9%;
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Webste
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                                                                                                                                                                                                                                                       US-08-880-342-27
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STATE: C
COUNTRY:
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                                                                 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAG 1366
                                                                                                                                                       1367 ACTIATGITAACGGCCTCAACGCTGCCGAGGAGATACTCGGCCGCTGTGGGCAAGGAG 1426
                                0;
                                                                                                           1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAG 1366
                                                                                                                                                                                                  103 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGAGGAGCGTTGGCCAAGGGA 162
                                0; Gaps
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EMBL #X59445
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US-08-35-486A-27

Sequence 27, Application US/08365486A

Patent No. 5834306

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: Deflinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
Best Local Similarity 66.9%; Pred. No. 5.5e-12;
Matches 103; Conservative 0; Mismatches 51; Indels
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Pred. No. 7.2e-12;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILN RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charlee K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                              1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                          163 GATGTTACAGCCCAGACAGCTCTTCAGCCTGCAC 196
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TELECOMPUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPKX: (415) 324-080
TELEPKX: (415) 324-080
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 66.9%;
Matches 103; Conservative
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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229 GCCTACGTGAACAACCTGAACGTCAACGAGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 288
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                                                                                                                                                                                                                                                                                                               APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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FILING DATE:
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US-09-075-019-8
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                                                                        1367 ACTIVICITAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAG 1426
GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCACGAGCACCATCAG 1366
                                     GCCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTGCACCACACGAAGCACCACGCG 228
                                                                                                            229 GCCTACGTGAACBACGTCAACGAGAGAAGTACCAGGAGGCGTTGGCCAAGGGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/126,109 FILING DATE: 30-UUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 72.4; DB 3; illarity 66.9%; Pred. No. 7.2e-12; Conservative 0; Mismatches 51;
                                                                                                                                                     1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                           289 GATGTTACAGCCCAGATAGCTCTTCAGCCTGCAC 322
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APPLICATION NUMBER: US 60/655,092
FILING DATE: 30-UUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKnown
FILING DATE: 03-MAR-199
ATTONREY/AGENT INFORMATION:
NAME: MCANILIAIN, Nabeela R.
REGISTRATION NUMBER: P-43,363
REGISTRATION NUMBER: P-43,363
REFERNICE/DOCKET NUMBER: UTSD:560
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                               Thigpen, Anice
Hohmeier, Hans-Ewald
Newgard, Christopher B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        US-09-126-109-1; Sequence I, Application US/09126109; Patent No. 6171856; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Unger, Roger H.
Shimabukuro, Michio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 976 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen, Guaxun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arno
STREET: P.O. Bo
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Техав
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houst
STATE: Texa
COUNTRY: US
ZIP: 77210
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCACCAAGCACCATCAG 1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 eccciedaaccicacaitaaacececacaitaiteacacicecacacacacacacacacaca 645
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                                                                          1367 ACTTATGTTAACGGCCTCAACGCTGCCGAGGAGGCTACTCGGCCGCTGTGGGCAAGGAG 1426
Sequence 8, Application US/09075019
Sequence No. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: A UPPERCOXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1427 GAIGIGCITACCCAGGITAAGCIICAGICIGIAC 1460
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                                                                                                                                                                             1427 GAIGIGCTIACCCAGGITAAGCTICAGICTGTAC 1460
                                                                                                                                                                                                                           323 GATGTTACAGCCCAGACAGCTCTTCAGCCTGCAC 356
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Pred. No. 2e-11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sheridan Ross P.C.
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KOVAZIK, JOSEQP B.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-928-692-29
; Sequence 29, Application US/08928692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 865-0223
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 3789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.9
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: CDNA
US-09-075-019-8
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Gaps . 0

Indels

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COMPUTE: IN PC compatible
COMPUTE: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 494
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3300 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                        FILING DATE:
                                           10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1341 CCCTTCACCACCAAGCACCATCAGACTTATGTTAACGGCCTCAACGCTGCCGAGGAGA 1400
                                                                                                                                                                                                               No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             912 AGCTTCACCACAAAAACACCACCAGACCTATGTCAACAGCTACAACACGCCATCGAAC 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              !: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      852 TTGACTGAATAACAGATGACTATGGCGCCCTTGAGCCCTCTATCTCCGGAAAGATCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                           APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
TITLE OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 3300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.0%; Score 71; DB 2; Length 330 Best Local Similarity 62.9%; Pred. No. 5e-11; Matches 110; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           CORREATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMNUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09339972
Patent No. 6323002
                                                                                                                                                                                                                                          405 Lexington Avenue
                                         Brody, Howard
Yaver, Deborah S.
Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3300 base pairs
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                           USA
Patent No. 5958727
                                                                                                                                                                                                                                                                                                                               10174
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                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-339-972-29
                                                              APPLICANT:
                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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1341 CCCTICACCACACCAAGCACCATCAGACTTATGTTAACGGCCTCAACGCTGCCGAGGAGA 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brown, Robert
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
ATITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 45
CORRESSEDONDENCE ADDRESS:
ADDRESSED: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1281 TTGGTTGAAAATTCCTCTCCACTCAGGCCCTGGAGCCCTCCATCTCCAAGGAGATCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912 AGCTTCACCACACACCACCACCACCACCTATGTCAACACTACAACACCCCCATCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1401 GCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCCAGGTTAAGCTTCAGTC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          972 AGCTCCAGGAGGCCGTCGCCAAGGAGGACATCACCACTCAGATCAACCTCAAGCC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.0%; Score 71; DB 4; Length 3300; 62.9%; Pred. No. 5e-11;
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1367 ACTIATGITAACGGCCTCAACGCTGCCGAGGAGGCTACTCGGCCGCTGTGGGCAAGGAG 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 GCCTACGTGAACAACGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCAAAGGGA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

1.9%; Score 70.8; DB 2; Length 977;

Best Local Similarity 66.2%; Pred. No. 2.3e-11;

Matches 102; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 GATGTTACAGCCCAGACAGCTCTTCAGCCTGCAC 357
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CLark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/POCKET NUMBER: 00786/177001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/23-4123
TELEPHONE: 617/723-4962
TELEPK: 617/723-8962
TELEPK: 617/723-8962
TELEPK: 617/723-8962
TELERK: 617/723-8962
TELERK: 617/723-8962
TELERK: 617/723-8962
TELERK: 617/723-8962
TELERGH: 977 base pairs
TERGHTH: 977 base pairs
TUPPE: nucleic acid
TUPPE: nucleic acid
TUPPOLOGY: linear

HOLDCOLOGY: linear

WOLECULE TYPE: DNA
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0;

Search completed: April 1, 2004, 13:45:30 Job time : 266.87 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

April 1, 2004, 10:57:14 ; Search time 47.1302 Seconds

(without alignments) 7877.372 Million cell updates/sec

US-09-727-855B-4 669

Title: Perfect score:

1 atgicigiticgageateeet......gatigeaggeigeietetaa 669 Sequence:

Scoring table:

682709 segs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5. Appli	0.0			' -		Patent No. 5240847		27		ìc	10	ı a	· -		هٔ د	S S	Datout No. 524084/		0 1	9	Š.	Patent No. 5240847	Patent No. 5240847	nce	90 annarma		
SUMMARIES	ID	US-09-091-097-5	US-09-091-097-7	-091-0	08-927-230A-	-09 - 151	09-023	10847-2	US-08-365-486A-27	880-345	US-09-126-109-1	US-08-023-980B-2	-08-486-953A-	US-09-075-019-8	-09-075-019-	9-610-520-60-SD	19	240847-9	5240847-17	1	0-2004		1 1 1 0 0 7 0	524U847-1	406	-08-928-692-	-09-339-972-	-214-909-	4
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40	Query	37.7	37.5	33.0	29.8	29.8	29.8	29.6	29.3	29.3	29.3	29.1	29.1	29.1	29.0	29.0	27.6	27.3	27.3	27.3	27.1	α 40	0.70	0 · ·	23.5	23.3	23.3	23.0	21.2
	Score	252	20	20	9	9	9	97	96	96	96	94	194.6	94	194	194		182.8	182.8	182.8	181.2	165.6	165.6		4.751	155.8	155.8	154	142
	Result No.	П	7	m	4	S	9	7	Φ,	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	1 6	6.0	24	25	56	27

NAME/KEY: CDS LOCATION: 1..618

28 139.2 20.8 4403765 3 US-09-103-840A-2 39 139.2 20.8 4411529 3 US-09-103-840A-1 31 134.6 20.1 1230025 4 US-09-139-731-1 32 123.8 18.5 491 1 US-09-139-489-603A-5056 34 121.8 18.2 654 4 US-09-198-489-003A-5056 35 121.6 18.2 491 1 US-09-489-003A-6999 36 119.6 17.9 624 4 US-09-252-991A-8022 37 119.6 17.9 999 4 US-09-252-991A-8294 38 117.4 17.5 491 1 US-08-133-711-37 40 111.2 16.7 491 1 US-08-133-711-37 41 112 16.7 491 1 US-08-133-711-34 42 111.1 16.6 491 1 US-08-133-711-38 43 110.4 16.5 491 1 US-08-133-711-38 44 111 16.6 491 1 US-08-133-711-38 45 110.4 16.5 491 1 US-08-133-711-38	Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 44, Appl		Sequence 8024, Ap Sequence 8294, Ap Sequence 36, Appl Sequence 37, Appl	Sequence 34, Appl Sequence 32, Appl Sequence 32, Appl	, w w w
28 139.2 20.8 30 139.2 20.8 31 134.6 20.8 31 134.6 20.1 32 121.8 18.2 121.6 18.2 35 119.6 17.9 36 117.4 17.5 39 114.2 17.1 41 11.2 16.7 43 111.1 16.6 44 111.1 16.6 5.5	US-09-103-840A-2 US-09-103-840A-1 US-09-373-731-1	: US-09-198-452A-1 US-08-133-711-44 US-09-489-039A-5056	US-09-489-039A-4999 US-08-133-711-40 US-08-253-061A-0022	US-09-252-991A-8294 US-09-252-991A-8294 US-08-133-711-36 US-08-133-711-37	US-08-133-711-34 US-08-133-711-32 US-09-262-856A-8	US-08-133-711-38 US-08-133-711-39 US-08-133-711-33
28 139.2 20.8 30 139.2 20.8 31 134.6 20.8 31 134.6 20.1 32 121.8 18.2 121.6 18.2 35 119.6 17.9 36 117.4 17.5 39 114.2 17.1 41 11.2 16.7 43 111.1 16.6 44 111.1 16.6 5.5	E E 4	4 4	4 1 4	444	H H 4	ਜਜਜ
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ALIGNMENTS

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APPLICANT: VARGINARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: NUSAHITI YOSHIMI
APPLICANT: AKIYAMA, KAZUO
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUBA, HIROSHI
APPLICANT: YANGUCHI, HIDEYO
TITLE OF INVENTION: MAIASSEZIA
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, SIEWART, KOLASCH & BIRCH, LLP
                                                                                                                                                                                                                                                                                                                                                                                               CITY: FALS CHURCH
STATE: VA
COUTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 5:
               Sequence 5, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
                                                                                   TAKESAKO, KAZUTOH
                                                                                                     OKADO, TAKASHI
YAGIHARA, TOMOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
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ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,1
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TYPE: nucleic acid
STRANDEDNESS: double
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LENGTH: 728 base pairs
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APPLICANT:
US-09-091-097-5
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FILING DATE
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US-09-091-097-29
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LOCATION:
US-09-091-097-7
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                                                                            TCAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCA 127
                                                                                                                                TCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAGACTTATGTTAACGGCC 187
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                                                  Gaps
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                      DB 4; Length 728
                        Score 252; DB 4; Length 72
Pred. No. 5e-68;
0; Mismatches 200; Indels
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VENTION: ANTIGENIC PROTEIN ORGINATING
VENTION: MALASSEZIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH,
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09091097
Patent No. 6432407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OKADO, TAKASHI
YAGIHARA, TOWOKO
KURODA, MASANOBU
ONISHI, YOSHIMI
AKTYO, IKUNOSHIN
AKIYAMA, KAZUO
YASUEDA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKESAKO, KAZUTOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                          37.7%;
                          Query Match
Best Local Similarity 65.5
Matches 385; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: TAKESA
APPLICANT: OKADO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-09-091-097-7
US-09-091-097-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 CGTGGGAGCACGCGTTCTACCTGCAGTACAAGAACGTCAAGGCCGACTACTTCAAGGCGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccaadracaccidecceccecitecenaciacececececeaeceaeceaeceaeceaecece 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 gcciadanciandancacachacanadadciacacacachacanchacaachadaaca 191
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
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Pred. No. 1.4e-67;
); Mismatches 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-205-8000
TELEPHONE: 703-205-8050
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63.9%;
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Best Local Similarity 63.9
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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478 ACTAAGAAGCTGGAAGTCACCACGACGCCAACCAGGACCCTCTGCTTACTCACATTCCT 537
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                                                                                                                                                                                                                                                                                                                                               481 GACTACTICAAGGCGAICIGGACGIGAICAACITTGAGGAGGCCGAGAAGGGTCICANG 540
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                                                                                                                                                                                                                                                                           538 ATCATCGGAGTIGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCT
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Sequence 1, Application US/08927230A

Patent No. 5985633

Patent No. 598563

PAPLICANT: Nick et al.

TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants

NUMBER OF SEQUENCES: 1.

CORRESPONDENCE ADDRESS:

ADDRESSEB: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street, Floor 24

CITY: Boston
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APPLICATION NUMBER: US/08/927.230A
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Pred. No. 9.2e-52;
0; Mismatches 216;
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INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
; TYPE: nucleic acid
TYPE: nucleic acid
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ilarity 61.1%;
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ATTORNEY/AGENT INFORMATION:
NAME: REMIlland, Jane
REGISTRATION NUMBER: 38, 8
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 367; Conserva
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ZIP: 02109-1875
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LOCATION:
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US-08-927-230A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
TITLE OF INVENTION: MALASSEZIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/09/091,097
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
33.0%; Score 220.6; DB 4;
Best Local Similarity 62.5%; Pred. No. 2.3e-58;
Matches 343; Conservative 0; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: BIRCH, STEWART, KOLASCH & BIRCH,
: PO BOX 747
FALLS CHURCH
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Sequence 29, Application US/09091097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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REFERENCE/DOCKET NUMBER: 14,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                            YAGIHARA, TOMOKO
KURODA, MASANOBU
ONISHI, YOSHIMI
KATO, IKUNOSHIN
                                                                                                                     TAKESAKO, KAZUTOE
                                                                                                                                                                                                                                                                                                                                                                                        AKIYAMA, KAZUO
YASUEDA, HIROSHI
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ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
                                                                                                                                                                       OKADO, TAKASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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ZIP: 22040-0747
COMPUTER READABLE FORM:
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Best Local Similarity
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TOPOLOGY:
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                                                                                                                                            249 TAAGCTICAGICTGCICTCAAGTICAACGGAGGAGGACACAICAATCACICTGTICTG
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                                        CTCCAAGGAGATCATGACCCTTCACCACACCACCACCATCAGACTTATGTTAACGGCCT
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
...manT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Floor 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,230
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
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Patent No. 6107070
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 199.4; DB 3;
Pred. No. 9.2e-52;
0; Mismatches 216;
REFERENCE/DOCKET NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELECOMMUNICATION INPORMATION:
TELEFAN: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.8%;
61.1%;
                                                                                                                                                                       LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 61.1
Matches 367; Conservative
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US-09-023-655-1348
                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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LOCATION:
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CGCTGCTGTCCAAGGATCCGGATGGGGCTTGGCTTGAACCCCGCTTAACTAAGAAGCT 488
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                                                                                                                                                                                                                                      603 GCTGGGGATTGATGTGTGGGAGCACGCTTACTACTTCAGTATAAAATGTCAGGCCTGA
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                                                  483 Térrideréréchadécricaderredécridecrircarrangeancegagacaerr
                                                                                                                                            543 ACAAATTGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAGGCCTTATTCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; PARCHI NO. 5240847
; PAPLICANT: HECKL, KONRAD; SPEVAK, WALTER.OSTERWANN, ELINBORG
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INCRID;
;WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUFTWANN, RUDOLF
;TITLE OF INVENTION: HUMAN MANGANESE SUFEROXIDE DISMUTASE
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Pred. No. 3.2e-51;
0; Mismatches 217;
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                                                                                                 489 GGAAGICACCACGACCGCCAACCAGGACCCICIGC-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
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Pred. No. 9.2e-52;
0; Mismatches 216;
                APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DET
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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FILING DATE:
FILING DATE:
FLING DATE:
FLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 13-
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 61.1%;
Matches 367; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
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LIBRARY: GENBANK
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GENERAL INFORMATION:
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CLONE: 934710
US-09-023-655-1348
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GAAGAACTIGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA 368
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                                                                                                                      369 GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
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                                        189 CAACGCTGCCGAGGAGGTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Tissue Specific Hypoxia Regulated TITLE OF INVENTION: Therapeutic Constructs NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS:
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365,486
APPLICATION NUMBER: US 08/365,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-880-342-27; Sequence 27, Application US/08880342; Patent No. 6218179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
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MEDIUM TYPE: Floppy
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          CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGGCCTGA 599
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                                                                                                                                                                                                                                                                                         Sequence 27, Application US/08365486A
Sequence No. 5834306
GENERAL INFORMATION:
APPLICANT: Webbster, Keith A.
APPLICANT: Bishopric, Namette H.
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
RELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196.2; DB 2;
Pred. No. 9.7e-51;
0; Mismatches 218;

    Dehlinger & Associates
    Cambridge Avenue, Suite 250

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 29.3%;
al Similarity 60.7%;
365; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 61..729
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Best Local Similarity
Matches 365; Conserv
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                                                                                                                                                                       T 660
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                                                                                                                                                                                                                                                                      RESULT 8
US-08-365-486A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: Pa
                                                                                                                                                                       6.60
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FILING DATE: 3(
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STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: P.
       US-09-126-109-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 ACAAATIGCIGCIIGIICCAAAICAGGAICCACTGCAAGGAACAAGAGGCCIIATICCACI 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 GCTGGGGATTGATGTGTGGGAGCACGCTTACTACCTTCAGTATAAAATGTCAGGCCTGA 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 CAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 CTCCAAGGAGATCATGACCCTTCACCACCACCACCATCAGACTTATGTTAACGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 GAACGTCAACGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGAGTGTTACAGCCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
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                                                                                                                                                                                                                                                                                                                                                                    human manganese superoxide dismutase EMBL #X59445
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Pred. No. 9.7e-51;
0; Mismatches 218; Indels
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFRENCE/DOCKET NUMBER: 8255.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.7%;
Matches 365; Conservative
                                                                                                                                                                                 LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                          unknown
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Best Local Similarity
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LOCATION:
US-08-880-342-27
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                                                                                                                                                                              LENGTH:
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280 GAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGAGATGTTACAGCCCAGAC 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 CTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAGACTTATGTTAACGGCCT
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                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.2; DB 3;
Pred. No. 9.7e-51;
0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-UUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATTORNEY/AGBNT INFORMATION:
NAME: MCMillian, Nabeela R.
REGISTATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  3: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                  Chen, Guaxun
Rhodes, Christopher J.
Hugl, Sigrun R.
Cousin, Sharon
                                                                         Thigpen, Anice
Hohmeier, Hans-Ewald
Newgard, Christopher
Sequence 1, Application US/09126109
Patent No. 6171856
                                                                                                                                                   Unger, Roger H.
Shimabukuro, Michio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 60.79
Matches 365, Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                       APPLICANT: Thigpen
APPLICANT: Thigpen
APPLICANT: Nobmeie
APPLICANT: Noger,
APPLICANT: Unger,
APPLICANT: Shimsbul
APPLICANT: Shimsbul
APPLICANT: Rhodes,
APPLICANT: Rhodes,
APPLICANT: Hugl, S
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281 GAACGICACCGAGGAGAAGTACCAGGAGGCGTIGGCAAAGGAAGAIGTIACAGCCCAGAC 340
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                                                                                                                                                                                                                                                                                                                                                   GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCCAGAGGCCCCGATTGCAGGC 659
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                                                                                                                                                                                                      CTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAGACTTATGTTAACGGCCT
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                                                                                                                             CAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT
                                                                                                                                                                512 TGTTGGTGTCCAAGGCTCAGGTTGGGTTTGGTTTTCAATAAGGAACGGGGACACTT
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                                                                                          Gaps
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APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: TREATWENT AND PREVENTION OF DISEASES OF
CORRESPONDENCE 53
CORRESPONDENCE ADDRESS:
                                                      Length
                                                                                          Indels
                                                    Score 194.6; DB 2;
Pred. No. 3e-50;
0; Mismatches 219;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                    29.1%;
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                                                                                          Conservative
 DNA
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                                                      Query Match
Best Local Similarity
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STREET: 1,
TMV: Boston
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US-08-023-980B-2
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                                                                         Best Local Sim
Matches 364;
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                                                      GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ER: 00786/177001
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FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
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APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND
TITLE OF INVENTION: TREATMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: Clark & Elbing LLP
STREET: 585 Commercial Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGIGSTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/723-4123
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LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEX:
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US-08-023-980B-2
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ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
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NAME: KOVATIK, JOSEPh E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3789 base pairs
                                                                            Sequence 8, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
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Best Local Similarity 60.4%;
Matches 365; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 194.6; DB 2; Length 60.6%; Pred. No. 3e-50; rive 0; Mismatches 219; Indels
                                                                                                                                                                                                NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/223002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
TELEFAX: 617/428-7045
                                                         APPLICATION NUMBER: US/08/486,953A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
ILBUGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.63
Matches 364; Conservative
                SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
OPERATING SYSTEM:
                                                                            FILING DATE: 07
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APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 GAATATGCATAAGCACCAGCCTCCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCA
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                                                                                                                                                                                                                                                                                                          ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
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376 GAGGAATCTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACACCGCTGCT 435
                                                                                                                                                                                                                                                                                                                                                                                                          GTCCAAGGATCCGGATGGGGCTGGCTTGGCTTGAACCCGGCTTACTAAGAAGCTGGAAGTC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- TTACTCACATTCCTATCGGA 546
61 CAGATCATGCAGCTGCACCACAGCAGCACCACGCGGCCTACGTGAACAACCTGAACGTC 120
                                                                                         121 acceaddagaagtaccagaggcgrrdgccaaggagargrracagccagacagcrcrr 180
                                                                                                                                                                                                                                                                         241 CTCAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGGAAGCCATC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                             352 GTCCAAGGCTCAGGTTGGGGTTGGGTTTCAATAAGGAACGGGGACACTTACAATT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 GCTGCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAGGCCTTATTCCACTGCTGGGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 GITGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGACCTGACTATCTC 606
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TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                               292 AAACGIGACTITGGIICCTITGACAAGIITAAGGAGAAGCIGACGGCIGCAICTGGII
                                                                                                                                        TIGGCICCTAIGGAICCGAGGAGGCIACCCICICIGAAGGACCICICAAGAAGGCIAIC
                                                 196 GCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCCTTACCCAGGTTAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 AAAGCTATTTGGAATGTAATCAACTGGGAGAATGTAACTGAAAGATACATGGCT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607 GCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCCGATTGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 ACCACGACGCCAACCAGGACCCTCTGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kovarik, Joseph E. REGISTRATION NUMBER: 33,
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 80203
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US-09-075-019-6
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                                                                                                                                                                                                                                 TGACTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCGATTGCA 656
    891 ATCTGTTGGTGTCCAAGGCTCAGGTTGGGGTTGGCTTTGGTTTCAATAAGGAACGGGGACA 950
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APPLICANT: UTC IR459
TILLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                   CACATTCC
                                                                                                                                          537 IATCATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 194; DB 3; Length 594;
Pred. No. 3.7e-50;
0; Mismatches 215; Indels
                                                 486 GCTGGAAGTCACCACGACCGCCAACCAGGACCCTCTGCTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sheridan Ross P.C.
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KOVALIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09075019 Patent No. 6190658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%;
Best Local Similarity 60.8%;
Matches 361; Conservative (
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TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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US-09-075-319-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                          Query Match 29.0%; Score 194; DB 3; Length 681;
Best Local Similarity 60.8%; Pred. No. 3.9e-50;
Matches 361; Conservative 0; Mismatches 215; Indels 18; Gaps
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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
US-09-075-019-6
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Search completed: April 1, 2004, 13:45:43 Job time : 60.1302 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 1, 2004, 08:33:07; Search time 257.583 Seconds (without alignments) 11033.514 Million cell updates/sec Run on:

US-09-727-855B-4 Title:

1 atgtetgttegageateeet......gattgeaggetgetetetaa Perfect score: Sequence:

699

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database

geneseqn2001as:*
geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:* geneseqn2003bs:*
geneseqn2003cs:*
geneseqn2004s:* genesegn1980s:* genesegn1990s:* genesegn2000s:* 9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ℴሎ				
Result No.	Score	Query Match	Length	DB		Description
1	252	37.7	728	2	AAT85876	Aat85876 Malassezi
7	250.6	37.5	812	N	AAT85877	
Э	220.6	33.0	630	~	AAT85894	
4	211.4	31.6	897	6	ADD35245	
Ŋ	205	30.6	1492	9	ABK63720	
9	205	30.6	1492	σ	ADB58236	Adb58236 Toxicity-
7	203.4	30.4	1438	3	AAA75734	
80	199.4	29.8	813	Н	AAN81158	_
σ	199.4	29.8	813	N	AAQ53193	
10	199.4	29.8	813	N	AAT15589	Human
11	199.4	29.8	813	7	AAT34277	Human
12	199.4	29.8	813	N	AAX24998	Aax24998 Human nat
13	199.4	29.8	813	m	AAA63891	
14	197.8	29.6	813	Н	AAN71370	
15	197.8	φ.	849	9	ABN84891	Abn84891 Human man
16	197.8	29.6	849	ø	ABA94453	Aba94453 Human man
17		29.6	972	7	ABX63836	
18	197.8	ė,	1026	9	ABL66512	Abl66512 Lung canc
19	197.8	29.6	1026	φ	ABK84524	Abk84524 Human cDN
20		9.	1046	7	AAQ94284	Human
21	197.8	٠	2504	4	AAL26545	Human
22	196.2	29.3	696	N	AAT31018	
23	196.2		916	N	AAQ67474	Human

Aax33940 Human HCM	Aax08429 Human man	Abz83721 Toxicolog	Aaf14076 Aspergill	Aav45115 A. fumiga	Aav73824 Human SOD	Aaz39782 Plasmid p	Aaz39779 Human man	Aaq20194 Mn-SOD (I	Aaq70431 MHS:MnSOD	Aaz39781 Human man	Ade76309 Human BSK	Abt09580 Phase-1 R	Aag70432 MHS2:MnS0	Abn98977 Arabidops	Aac51219 Arabidops	Aac40144 Arabidops	Ade25718 Human cDN	Aan81224 cDNA of f	Aaq94277 Human man	Abz56304 Aspergill	Aan81225 cDNA of f
AAX33940	AAX08429	ABZ83721	AAF14076	AAV45115	AAV73824	AAZ39782	AAZ39779	AAQ20194	AAQ70431	AAZ39781	ADE76309	ABT09580	AAQ70432	ABN98977	AAC51219	AAC40144	ADE25718	AAN81224	AAQ94277	ABZ56304	AAN81225
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29.3	29.3	29.3	29.3	29.2	29.1	29.1	29.0	29.0	29.0	29.0	28.9	28.9	28.5	28.1	28.1	28.1	27.7	27.6	27.6	27.5	27.3
196.2	196.2	196.2	195.8	195.2	194.6	194.4	194	194	194	194	193.6	193.4	190.8	188	188	188	185.4	184.4	184.4	184.2	182.8
24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Malassezia fungus MF-3 antigenic protein encoding cDNA. AAT85876 standard; cDNA to mRNA; 728 BP. (revised)
(first entry) allergy; antigen; ds. 27-AUG-2003 23-FEB-1998 AAT85876; **AAT85876**

Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody; /product= "MR-3_antigenic_protein" Location/Qualifiers ø /*tag= Malassezia. Key

96WO-JP003602 WO9721817-A1 10-DEC-1996; 19-JUN-1997

95JP-00346627. 96JP-00257612. 96JP-00257613. 12-DEC-1995; 05-SEP-1996; 05-SEP-1996; (TAKI) TAKARA SHUZO CO LTD

Kato I; Onishi Y, Kuroda M, Takesako K, Okado T, Yagihara T, I Akiyama K, Yasueda H, Yamaguchi H;

WPI; 1997-332788/30. P-PSDB; AAW29770.

Antigenic proteins from the fungus Malassezia - bind to IgE antibodies present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.

Claim 53; Page 76-77; 162pp; Japanese.

The present sequence encodes a specifically claimed antigenic protein

/product= "MR-4_antigenic_protein"

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WO9721817-A1
                                                                10-DEC-1996;
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05-SEP-1996
                                           19-JUN-1997
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isolated from the fungus Malassezia. The antigenic protein can bind to IgE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be used in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AVG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                 GGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGA
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6.6e-66;
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65.5%; Pred. No. 6.6e
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AGGAGATCATGACCTTCACCACACCACCATCAGACTTATGTTAACGGCCTCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCGAGGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCCAGGTTAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 27-AUG-2003 to correct OS field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 812 BP; 235 A; 245 C; 218 G; 114 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onishi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250.6; DB :
Pred. No. 1.8e-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuroda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 56; Page 77-78; 162pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yagihara T,
Yamaguchi H;
                                                                                                                95JP-00346627.
96JP-00257612.
96JP-00257613.
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96WO-JP003602
                                                                                                                                                                                                                                                                                                                                                            LTD.
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                                                                                                                                                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okado T,
Yasueda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997-332788/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.pachydermatitis).
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TCTCTGTTCTGGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidative stress; apoptosis; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kerstann K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001; 2001US-0316323P. 31-AUG-2001; 2001CA-02356540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0-AUG-2002; 2002WO-US027886
                                                                                                                                                                                                                                                                                                                                                                                                                                                         897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD35245 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-300821/29
                                                                                                                                                                                                                                                                                                                                                          GCTGCTCTC
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              298
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              611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a PCR amplification fragment of the MF-4 antigenic protein isolated from the fungus Malassezia. The antigenic peptide can bind to IgB antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be used in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic proteins from the fungus Malassezia - bind to IgE antibodies present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.
                                                                                                                                                                                                                                                               Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
allergy; antigen; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 GAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACACCAAGCACCATCAGACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAACCTGCTTTCTGGGGGGGGATAATGGAGGACGCACTACGAGGAGGACCACCGCACCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GTTAACGGCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 Grchachacterghacecececedadehochacerearceacececrececaceacecee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTGGGAGCACGCGTTCTACCTGCAGTACAAGAACGTCAAGGCCGACTACTTCAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             Malassezia fungus MF-4 antigenic protein PCR amplification fragment.
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                                          TTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCGATTGCAGGCTGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 630 BP; 156 A; 191 C; 180 G; 101 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.0%; Score 220.6; DB 2 62.5%; Pred. No. 2.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuroda M,
                                                                                                                                            ВР
                                                                                                                                            AAT85894 standard; cDNA to mRNA; 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Page 99; 162pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yagihara T,
Yamaguchi H;
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                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okado
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                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1996;
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                                                                                                                                                                                                 27-AUG-2003
23-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1997
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                                                                                                                                                                                                                                                                                                                  Malassezia.
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Matches
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The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial blology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
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                                                                                                                                                                                                                           CCTCTCAAGAAGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse mitochondrial DNA sequence SEQ ID NO:3025
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ce the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid relative to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such organisms, which are useful for determining expression profiles diagnostic of energy metabolism-related physiological conditions, identifying biochemical diagnostic of energy metabolism-related physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, identifying and identifying and identifying and identifying and identifying and identifying and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also disease, as well as distinging disinced disorders that result from conditive or adefining expression signatures or profiles for mitochondrial disorders that result from conditive or physhology. Avefunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD31224-ADD3526 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
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357 428 648 128 188 237 248 297 308 408 488 599 CAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT ccederadades de contración de c CTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAGACTTATGTTAACGGCCT 178 TAACGCGCAGATCATGCAGCTGCACCACCAAGCACCATGCGGCCTACGTGAACAACCT CAACGCTGCCGAGGAGAGGTACTCGGCCGCTGTGGGCAAGGAGGATGTGCCTTACCCAGGT CAACGCCACCGAGGAGAAGTACCACGAGGCTCTGGCCAAGGGAGATGTTACAACTCAGGT cacrcrrcaccacrasagrrcaarsgrsssscararraarcacaccarrrrcrs GAAGAACTIGGCTCCCTAIGGAICCGAGGAGGCIACCCICTCIGAAGGACCTCICAAGAA -----AAGGAGAGTTGCTGGA GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC GGCTATCAAGCGTGACTTTGGGTCTTTTGAGAAGTTTAAGGAGAAGCTGACAGCCATGTC CGCTGCTGTCCAAGGATCCGGATGGGGCTGGCTTGAACCCCGCTTACTAAGAAGCT 469 reredeadricaaderradecredecrederrederradaraadeacaaderecerr --TTACTCACATTCCTAT 529 ACAGATTGCTGCTGCTCTAATCAGGACCCATTGCAAGGAACAACAGGCCTTATTCCGCT CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGA 589 GCTGGGGATTGACGTGTGGGAGCACGCTTACTACCTTCAGTATAAAAACGTCAGACCTGA Gaps 18; Length 897; Sequence 897 BP; 225 A; 214 C; 247 G; 211 T; 0 U; 0 Other; Indels Score 211.4; DB 9; Pred. No. 1.5e-53; 0; Mismatches 196; GACAAACCTGAGCCCTAAGGGTGGTGGAGAACCTA GGAAGTCACCACGACGCCAACCAGGACCCTCTGC 31.6%; Local Similarity 63.2%; hes 367; Conservative 69 118 129 189 238 298 309 358 369 409 429 489 Query Match Matches

toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the

toxicity markers

600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640

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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes and predict cellular pathways that a compound modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of and a user interface to view the information used to present information and a tissue or cell sample exposed to a persent information and a tissue or cell sample exposed to a persent information and a tissue or cell sample exposed to a persent information and a tissue or cell sample exposed to a persent information and a tissue or cell sample exposed to a persent information and a present information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic effects of compounds or the progression of these toxic determining the changes in gene expression in tissues or cells the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                Rat sequence differentially expressed in response to a hepatotoxin #1627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as
                                                                                                                                                                                                                                                                                         hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elashoff MR;
                                                                                                                                                                                                                                                                                         Rat; ss; hepatotoxin; expressed sequence tag; EST; drug scr
differential expression; centrilobular necrosis; steatosis.
Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1627; 239pp; English.
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                                                                                                                      ABK63720 standard; cDNA; 1492
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2001US-0292336P.
2001US-0295798P.
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2001US-0290029P.
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2001US-0298884P.
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22-MAY-2001;
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11-MAY-2001;
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prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Heparotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a heparotoxic agent
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                                                                                                                       Length 1492;
                                                                                           Sequence 1492 BP; 380 A; 328 C; 392 G; 392 T; 0 U; 0 Other;
                                                                                                                                                    0; Mismatches 200; Indels
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Pred. No. 1.7e-51;
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62.5%;
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Best Local Similarity 62.5'
Matches 363; Conservative
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The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile cat a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect. The compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the pression are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence date for this patent did not form part of the printed.

Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.

Claim 1; SEQ ID NO 3262; 1156pp; English

Elashoff

ď Castle

Higgs B,

Johnson K,

Porter M,

Mendrick D,

WPI; 2003-689530/65

(GENE-) GENE LOGIC INC

2002US-00060087, 2002US-0364045P, 2002US-0364055P, 2002US-0436643P,

15-MAR-2002; 15-MAR-2002; 31-JAN-2002;

30-DEC-2002;

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Pred. No. 1.7e-51;
0; Mismatches 200; Indels
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31-JAN-2003; 2003WO-US003194.

07-AUG-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGA
                                                                    129 CTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAGACTTATGTTAACGGCCT
                                                                                                                                     189 CAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                          CGCTGCTGTCCAAGGATCCGGATGGGGCTGGCTTGGACCCGCTTACTAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 GGAAGTCACCACGACCGCCAACCAGGACCCTCTGC-----TTACTCACATTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crarcigaaagccarirggaargraarcaactgggagaarg 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding human manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nimrod A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-00032734.
88US-00161117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88EP-00104880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1988-272584/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1988
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AAN81158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes the use of a recombinant adeno-associated virus (rAAV) composition. The rAAV comprises a polynucleotide sequence encoding a mammalian catalase or superoxide dismutase polypeptide to reduce demyelination in an optic nerve. The rAAV are useful for scavenging reactive oxygen species in a mammal suspected of having optic neuritis, to reduce the effects of demyelinating disease in a mammal and prophylactically used to suppress blood brain barrier disruption in a mammal having identified allergic encephalomyelitis. The rAAV composition is useful for reducing symptoms associated with demyelinating diseases such as optic neuritis, multiple sclerosis, allergic encephalomyelitis, where the symptoms associated with these disease include optic disk edema, increase of optic nerve cell count, disruption of blood brain demyelination of axons. The present sequence is expressed using the rAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
545 ACAGATTGCCGCCTGCTCTAATCAGGACCCACTGCAAGGAACCACAGGCCTTATTCCACT 604
                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus, catalase, superoxide dismutase, demyelination, optic nerve, reactive oxygen species; optic neuritis, optic disk edema, demyelinating disease, allergic encephalomyelitis, multiple sclerosis; allergic encephalomyelitis, blood brain barrier, ss.
                               540 CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGA
                                                                 605 GCTGGGGATTGATGTGTGGGAGCACGCTTACTATCTTCAGTATAAAACGTCAGACCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of recombinant adeno-associated virus composition for treating demyelinating disorders e.g. multiple sclerosis and allergic encephalomyelitis, comprises viral constructs expressing catalase or
                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of a manganese superoxide dismutase (Mn SOD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGAGG 640
                                                                                                                                   CTATCTGAAAGCCATTTGGAATGTAATCAACTGGGAGAATG 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 203.4; DB 3;
llarity 62.3%; Pred. No. 5.1e-51;
Conservative 0; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 78pp; English.
                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                    AAA75734 standard; DNA; 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2000; 2000WO-US006839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0124398P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QI X.
HAUSWIRTH W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                superoxide dismutase.
                                                                                                                                                                                                                                                                                     (first
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Matches 362; Conserv
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(HAUS/)
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MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion; injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
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Matches
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                                                                                          is inserted
                                                                                                                                                                                                                                                                                                                                                                  GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                        348 GACAAACCTGAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                             GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 GGAAGTCACCACGACCGCCAACCAGGACCCTCTGC------TTACTCACATTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 acaaatrgcrgcrrgrccaaarcaggarccacrgcaaggaagaagaaggccrrafrccacr
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                                                                                                                                                                                                                                                       189 CAACGCTGCCGAGGAGGTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT
                                                                                                                                                                    Gaps
                       Recombinant human manganese superoxidedismutase - used for treating reperfusion injury, inflammation, arthritis, bronchial pulmonary dysplasia or lung fibrosis.
                                                                                                                                                                    18;
                                                                                                                                               Length 813;
                                                                                          and
                                                                                                                          Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                    Indels
                                                                                          The cDNA encodes human manganese superoxide dismutase, into a plasmid, eg pMSE-4 (ATCC 53250)
                                                                                                                                              Score 199.4; DB 1;
Pred. No. 6.4e-50;
0; Mismatches 216;
                                                                     Disclosure; Page ?; 46pp; English
                                                                                                                                               29.8%; al Similarity 61.1%; 367; Conservative
      P-PSDB; AAP80551
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                                                                                                                                                Query Match
Best Local Si
Matches 367
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BP.

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CDNA;

AAQ53193 standard;

RESULT 9

AAQ53193;

(revised)
(first entry)

25-MAR-2003 21-JUN-1994

AAQ53193
ID AAQE
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AC AAQE
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DT 25-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAAACCTCAGCCCTAACGGTGGTGGAACCCA-----AAGGGGAGTTGCTGGA 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence encodes a maganese superoxide dismutase which can be used t catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide and molecular oxygen. It can be used to reduce reperfusion injury following ischaemia and prolong the survival of excised organs. It can also me used as a long acting anti-inflamatory drug. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 gaacercacceaedadaagraccaedaeecerreeceaedadeaearerracceeceaer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 CAACGCTGCCGAGGAGACTACTCGCCCGCTGTGGGCAAGGAGGATGTGCCTTACCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 CICCAAGGAGATCATGACCCITCACCACACACACCACCATCAGACTTAIGTTAACGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression plasmid in Escherichia coli host system - encodes human manganese superoxidedismutase analogue, useful for e.g. treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 199.4; DB 2; Length 813;
Pred. No. 6.4e-50;
0; Mismatches 216; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                       iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1a-1c; 27pp; English.
                                                                                                           /product= "MnSOD"
                                                                                                                                                                                                                                                                                                    85US-00801090.
86US-00907051.
86IE-00002851.
87US-00032734.
89US-00453057.
                                                                                                                                                                                                                                                         92US-00912213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 29.8%; al Similarity 61.1%; 367; Conservative
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                                                                                                                                                                                                                                                                                                    22-NOV-1985;
12-SEP-1986;
29-OCT-1986;
27-MAR-1987;
Homo sapiens
                                                                                                                                                                                                                                                         10-JUL-1992;
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                                                                                                                                                                                                               14-DEC-1993
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gt10 in Escherichia coli, by screening with a 5'-probe (AAT15591) and a 3'-probe (AAT15522). The sequence of the insert in plasmid pMS8-4 (Obtained by subcloning in plasmid pBR322) is shown. The cDNA may be expressed in e.g. E. coli for production of recombinant MASOD. The MMSOD product may be cleaved with Aeromonas proteolytica aminopeptidase to produce an N-terminally truncated analogue with lysine and optionally histidina residues removed. The MMSOD analogue may be used in therapy of conditions associated with generation of coxygen free radicals, particularly synovial inflammation, arthritis and lung fibrosis (claimed). (Updated on 25-MAR-2003 to correct PF field.)
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es 216;
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Pred. No. 6.4e
0; Mismatches
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                                                                                                                                                                                                                                                          CTAICTCGCTGCTGTTTGGTCCGTTAICAACTACAAGGAGGCAGAGGCCCGATTGCAGGC
CGCTGCTGTCCAAGGATCCGGATGGGCTTGGCTTGAACCCGCTTACTAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA; Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning; aminopeptidase; antiinflammatory; oxygen free radical scavenger; synovial inflammation; arthritis; lung fibrosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Manganese superoxide-dismutase"
/note= "EC-1.15.1.1"
+1...14
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                                                                                   GGAAGTCACCACGACCGCCAACCAGGACCCTCTGC---
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                                            348 GACAAACCTCAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGGA
                                                                                GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant human manganese superoxide dismutase proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human native manganese superoxide dismutase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 52-53; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of recombinant human manganese super:oxide dismutase - for treating inflammation or bronchial pulmonary dysplasia, reducing reperfusion injury or prolonging organ survival.
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Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia; bronchial pulmonary dysplasia; inflammation; antiinflammatory; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 199.4; DB 2; Length Pred. No. 6.4e-50; 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A-1C; 27pp; English
                                                                                                                                                                                                                                                                                                                                    85US-00801090.
86US-00907051.
86IE-00002851.
87US-00032734.
89US-00453057.
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61.1%;
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93US-00120951
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                                                                                                                                       43. .114
/*tag= b
115. .708
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P-PSDB; AAW00018.
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Best Local Similarity
Matches 367; Conserv
                                                                                                                                                                                                                                                                                                                                      22-NOV-1985;
12-SEP-1986;
29-OCT-1986;
                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                       09-JAN-1995;
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(first entry)

04-DEC-2000

AAA63891;

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This cDNA sequence codes for human manganese superoxide dismutase (hMmSDD, see AAW98169). Novel MnSOD proteins having catalytic activity which differs from this natural hMmSOD are claimed. The modified proteins exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMmSOD. The modifications involve one or amino cid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163 (see also AAW9811-77). Nucleic acids encoding the modified hMmSOD proteins, or cypression vectors in which modified hMmSOD proteins, or promoter (preferably mammalian), can be used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to reat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed), he used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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AAA63891 standard; cDNA;

RESULT 13 AAA63891

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human manganese superoxide dismutase protein useful as antioxidant for treating cytotoxicity caused by superoxide radicals, inflammation and reperfusion injury following ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGAGATGTTACAGCCCAGAT
                                                                                    Human; manganese superoxide dismutase; hMn SOD; superoxide radical; superoxide radical damage; cytotoxicity; inflammation; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                  /*tag= a //transl except= (pos: 505. .507, aa: Xaa) //transl except= (pos: 511. .513, aa: Ala) /product= "manganese superoxide dismutase" //note= "Xaa is Gln or Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
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                                                         cDNA encoding a human manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 199.4; DB 3;
Pred. No. 6.4e-50;
0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reperfusion injury following ischemia
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llarity 61.1%;
Conservative (
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115. .708
                                                                                                                                                                                                                                                                           43. .114
                                                                                                                 reperfusion injury; ss.
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Local S.
367;
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New DNA coding for polypeptide of human manganese superoxidedismutase useful e.g. for treating inflammation, and new expression vectors and transformed cells.
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Local Similarity 60.9%;
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              639 TTATCTAAAAGCTATTTGGAATGTAATCAACTGGGAGAATGTAACTGAAAGATACATGGC
                                                                     348 GACAAACCTCAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGGA
                                                                                        369 GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
                                                                                                          399 AGCCATCAAACGTGACTTTGGTTCCTTTGACAAGTTTAAGGAGAAGCTGACGGCTGCATC
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                                                                                                                                                                  489 GGAAGTCACCACGACCGCCAACCAGGACCCTCTGC-
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12-SEP-1986;
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This purified cDNA encodes both prepro- and mature-manganese superoxide dismutase (MSOD). It is one strand of a double stranded molecule contained in a recombinant vehicle. The MSOD produced catalyses the reaction of hydrogen ions and the SOD radical anion to form hydrogen peroxide and water. It is useful in veterinary and pharmaceutical compsns. for e.g. reducing lesions of reperfusion following ischaemia, to prolong survival time isolated organs and for treating inflammation. See also ANY1371-72. (Updated on 10-MAR-2003 to add missing OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing recombinant human manganese superoxide dismutase, useful in the treatment of osteoarthritis and rheumatoid arthritis.
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                                                 Superoxide dismutase; SOD; hSODm; enzyme; human; osteopathic; antirheumatic; antiarthritic; vasotropic; antiinflammatory; gene; ss.
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Pred. No. 2e-49;
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                         Human manganese superoxide dismutase gene.
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                                                                                                                 Location/Qualifiers
                                                                                                                                                                                           "hSODm"
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April 1, 2004, 12:35:05; Search time 2584.54 Seconds (without alignments) 11219.210 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ok			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	Д	Description
1	699	100	ì	1	34	AX128479 S
2	699				1571	BD015713 Recombina
m	316.6	47.3	597	ψı	948	AX128481 Sequence
4, I	16.	٠.			BD015/14	AV423629 Crimtococ
ς V	294	<i>:</i> ~			A1423623 GMIT56403	U56403 Ganoderma m
0 [: ~			E15568	E15568 cDNA encodi
- 60	252	`.'			AR222757	Sequence
6	Ċ.	Α,			E15569	E15569 cDNA encodi
10	ċ	ς.			AR222758	AR222758 Sequence
11	'n.				AF114848	AFII4848 FAXILLUS
12	220.6	<u>.</u> .			6 AR222775	FISSE CONTRACTOR
L 7					E13303 MSV548421	AJ548421 Malassezi
# L	: 5				MMNSODRX	Z18857 M.musculus
16	1				MMNSODR	louse
17	080				BC018173	Mus
18	208.2				AB001693	AB001693 Equus cab
19	08.			10	BC010548	Mus
50	5 20	<u>.</u> .		ω (AY027564	Asper
21	207.6	_;;		20 0	AY206454	AIZU6434 COLUNCEDS
2 6	206	<u> </u>		2 0 0	KICSODACA	AK104160 Orvza sat
200	206			σ	AK104030	AK104030 Oryza sat
25	206			œ	AK070528	AK070528 Oryza sat
26	206	0		8	RICRMSO	L34038 Oryza sativ
27	206	0	•	œ	RICRMSOA	L34039 Oryza sativ
28	2	0	• •	9	AX401951	AX401951 Sequence
29	40	0		ω	AK119904	Oryza sat
30	203.4	0		10	RNMNSOD	YUU49/ KAT MKNA IO
31	200	5 (C		ه د	AKU86849	AD106627 Sequence
35	כי	20 0		، م	AKIU562/	ANTOROGY Sections
13. 13.	כי כי	<i>y</i> 0		ه م	HKSBUBUS	VOO472 Human mRNA
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41	97	σ			5392	53929 Sequend
42	97	d)			K09	197395 Homo
43	97	Q)			B08727	7277 Macaca
44	97	σ			8727	387278 Macaca

ALIGNMENTS

		linear PAT 15-MAY-2001					Phaffia rhodozyma)		cetes;	Cystofilobasidiales;				rticularly astaxanthin
		AX128479 669 bp DNA	Sequence 4 from Patent EP1111067.	AX128479	AX128479.1 GI:14134946		Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)		Eukaryota; Fungi; Basidiomycota; Hymenomycetes;	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;	Cystofilobasidiaceae; Xanthophyllomyces.	1	Hoshino, T., Ojima, K. and Setoguchi, Y.	percenting and production of carotenoids, particularly astaxanthin
RESULT 1	AX128479	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	TITI

27-AUG-2002

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The first statement of the following for the following f
                                                                                                                                                                                                                                                                                                                            in particular, astaxanthin
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Recombination production of carotenoids, in particular,
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/ Organism="Xanthophyllomyces dendrorhous"
/mol type="genomic DNA"
/db_xref="taxon:5421"
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Heterobasidiomycetes, Tremellomycetidae, Cystof
Cystofilobasidiaceae, Xanthophyllomyces.
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100.0%; Pred. No. 5.3e-168;
iive 0; Mismatches 0;
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Xanthophyllomyces dendrorhous
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Location/Qualifiers
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// Cyganism="Xanthophyllomyces dendrorhous"
// Ab_ type="unassigned DNA"
// Ab_ xref="taxon:5421"
// . .669
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Pred. No. 5.3e-168;
0; Mismatches 0;
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/note="unnamed protein product"
Patent: EP 1111067-A 4 27-JUN-2001;
F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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Ganoderma microsporum manganese-superoxide dismutase mRNA, complete
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                                                                                                                                                 ATCTCCAAGGAGATCATGACCTTCACCACCAAGCACCATCAGACTTATGTTAACGGC 186
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Aphyllophorales; Ganodermataceae; Ganoderma.
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Studies of Manganese-Superoxide Dismutase Gene of Ganoderma
Thesis (1996) National Talwan University, Talpei, Talwan, Republic
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Bubmitted (24-APR-1996) Huei-Fang Wang, Applied Microbiology
Laboratory/Agricultural Chemistry Department, National Taiwan
University, Taipei, Taiwan, Republic of China
12 (bases Ito 704)
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       Length 678;
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   Score 294; DB 8; I
Pred. No. 1.2e-67;
0; Mismatches 185;
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KGTKKLEITTTPNQDPLLSHVPTIGIDIWEHAFYLQYKNVKPDYLNAIMDVLNYEEAE
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tr. [bases 1 to 678)
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Omplete obna, Chaturvedi, V. and Chaturvedi, S. Complete obna of MnSOD of Cryptococcus neoformans var. grupublished
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(bararibura, S.D., Chaturvedi, V. and Chaturvedi, S. Direct Submission

Submitted (28-SEP-2003) Mycology, Wadsworth Cent
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                                            AACGCCGCTATCCAGGCTTTCTCCCAGACCAATGACATCAAGG-
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/organism="Cryptococcus
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Location/Qualifiers
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/db_xref="taxon:37769"
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TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 252; DB 6; Length 728; 65.5%; Pred. No. 2e-56; ive 0; Mismatches 200; Indels
     and Yamago,K., Daimon,H., Kuroda,M., Katou,I., Yasueda and Yamago,Ki., Daimon,H., Kuroda,M., Katou,I., Yasueda and Yamago,Ki.H.
RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GEN PARARA SHUZO CO LTD
OS Malassezia furfur
PN JP 1998077296-A/3
PD 24-MAR-1998
PF 05-SEP-1996 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANU

    . 728
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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EQNWGSYDPFKERFNATTAALGGSGWGWLGLNPATKRLEITTTANQDFLLSHVPIIGV
DIWEHAFYLQYINVKADYLAAIWIVINFKEAERRLIEATK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.7%; Score 258.8; DB 8; Length llarity 68.0%; Pred. No. 3.1e-58; Conservative .0; Mismatches 167; Indels
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cDNA encoding Malassezia antigen protein MF-3.
E15568
                                organism="Ganoderma microsporum"
                                                                                                         'db_xref="taxon:34462"
                                                                                                                                       34. ...636
/EC_number="1.15.1.1"
                                                      mol type="mRNA"
strain="RSH 0821"
                                                                                                                                                                                           'note="Mn-SOD"
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JP 1998077296-A/3.
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Takesako,K., Daimon,H., Kuroda,M., Katou,I., Yasueda,H., Akiyama,K. and Yamaguchi,H..

RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
PATENE: JP 1998077296-A 4 24-MAR-1998;
TAKARA SHUZO CO LID
OS Malassezia furfur
PN JP 19980772296-A/4
PD 24-MAR-1998
PF 05-SEP-1996 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI KATOU
                                                                                            PAT: 28-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product='Malassezia antigen protein MF-4'.
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CO7K14/195,A61K39/35,C07H21/04,C07K7/08,C12N15/09,C12Q1/68, PC
GO1N33/53,
PC GO1N33/569;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC mti-sense: No;
FH Key
FH Source 1. .812
/organism='Malassezia furfur' FT
FT
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Pred. No. 4.9e-56;
0; Mismatches 214;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Takesako, K., Okado, T., Yagihara, T., Kuroda, M., Onishi, Y., Kato, I., Akiyama, K., Yasueda, H. and Yamaguchi, H.
Antigenic protein originating in malassezia
Patent: US 6432407-A 13-AUG-2002;
Location/Qualifiers
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61 55	AFILABABLE AND ABOUNDED AND ABOUTHORS Jacob, C., Courbot, M., Botton, B. and Chalot, M. TITLE Cloning and sequencing of a full-length cDNA encoding the manganese superoxide dismutase precursor of the ectomycorrhizal fungus, Paxillus involutus and Chalot, M. Botton, B. and Chalot, M. 2 (bases 1 to 621) AUTHORS Jacob, C., Courbot, M., Botton, B. and Chalot, M. TITLE Direct Submission Joornal Solon (17-DEC-1998) Forest Biology, University H. Poincare, Vandoeurre 54506, France FEATURES FEATURES Jone AFILABABLE AND	· 4 th H	Oy 137 AGATCATGACCATCACCACACCATCAGACTTATACGGCTCAAGGCTG 196
Qy 434 CTGTCCAAGGATCCGGATGGGCTTGGCTTGAACCCGCTTACTAAGAAGTGGAAG 493 Db 432 GCATCCAGGACGGGCTGGGCTTGGCTTGACTCACACGAGAAGCTCGACA 491 Qy 494 TCACCCACGAGCGCGCAGGACCCTGCTTACTCCATACATCGGAGTTGACA 553 Db 492 TCATCACGACCGCCACACGGACCCGCTCCTGCTTACTCCTATCATCGAGTTGACA 551 Db 492 TCATCACGACCGCGAACCGGACCCGCTCCTGCTGCACAAGCCGACTACTGGATGATG 551 Db 554 TCTGGGAGCACGCTTTCTACCTTCAGTACAAAGCGCACAAGCCTGATTGCTGCTG 613 Db 552 CGTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAAGACTTCTAAAGGCGA 611 Qy 614 TTTGGTCCGTTATCAACAACAACAAGAACGTCCAAAGACCTCTC 666 Ch 611 TTTGGTCCGTTATCAACAACAACAAGAAGCCCGATTGCAACAACGTCTC 664	SULT 10 222758 AFCUST FINATION SECESSION ARESION AND CONCEDUS URCE 1 ORGANISM UT FERENCE 1 AUTHORS TA TITLE AR TITLE AR GOURNAL PR SOURCE GOURNAL PR AUGUST	Query Match 37.5%; Score 250.6; DB 6; Length 812; Best Local Similarity 63.9%; Pred; No. 4.9e-56; De-56; Matches 379; Conservative 0; Mismatches 214; Indels 0; Gaps 0; Qy 74 CAAAGCATACCCTGCCTGCGTACGCTTACGATACGACCTCCATCTCA 133 Db 72 CCAAGTACACGCTGCGTACGACTACGACTACGACCTCGAGCGATCTCGA 131 Qy 134 AGGAGATCATGGACCACCACCACCACCACCACCACCACCACCACCACCAC	372 TCGACCGCGACTTTGGCTCGGTCGACGCCATGAAGGAGAAGTTCAACGCGGCGCTCGCGG 434 CTGTCCAAGGACTGGATGGCTTGGCTTGGACCTGCGGG 435 GCATCCAGGGCTGGGGCTGGCTTGGCTTGAACCCCACGAGGAAGGTGGAAG 494 TCACCAGGACCGCCAACCAGGACCCTTACTTACTACTACTACTACATGGAAGGTTGACA 495 TCACCAGGACCGCCAACCAGGACCCTTACTTACTACATCCTATCATTGGATTGACA 497 TCACCAGGACCGCCAACCAGGACCCTTCCTTACTATCTAT

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halot,M.
yth cDNA encoding the manganese
e ectomycorrhizal fungus,
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INHSLEWRYLLAPASGKGKGGELKFGPLKD
GGMGIANPSTKELEIATTPNQDPLLTHIPII
INPKEAEKRFTEGLSGSKL"
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de dismutase precursor (MnSOD)
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GTCAAGCCTGACTATCTCGCTGCTG 613
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184; Indels 21; Gaps
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                                                      OB 8; Length 621;
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PAT 28-JUL-1999
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Takesako, K., Daimon, H., Kuroda, M., Katou, I., Yasueda, H., Akiyama, K.
and Yamaguchi, H.
    361 ACGCAGAAGCTCGACATCATCACGACCGCGAACCAGGACCCGCTCCTGTCGCACAAGCCG 420
                                                  ATCATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCT 597
                                                                                                                                                                                                                                                              481 GACTACTICAAGGCGAICTGGACCGIGAICAACTITGAGGAGGCCGAGAAGCGICICANG 540
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                                                                              ACTAAGAAGCTGGAAGTCACCACGACCGCCAACCAGGACCCTCTGCTTACTCACATTCCT
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CO7KL4/195,A61K39/35,C07H21/04,C07K7/08,C12N15/09,C12Q1/68,
G01N33/53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-1996 JP 1996257613
TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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TAKARA SHUZO CO LID
OS Malassezia furfur
PN JP 1998077296-A/20
PD 24-MAR-1998
PF 05-SEP-1996 JP 1996257613
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Pred. No. 5.3e-47;
0; Mismatches 198;
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/organism="unidentified"
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/db_xref="taxon:32644"
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strandedness: Double;
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hypothetical: No;
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ilarity 62.9%;
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Takesako, K., Okado, T., Yagihara, T., Kuroda, M., Onishi, Y., Kato, I.,
Akiyama, K., Yasueda, H. and Yamaguchi, H.
Antigenic protein originating in malassezia
Patent: US 6432407-A 29 13-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAGACTTAT 177
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AAGCTGCCCTCCGCTTCAACGGTGGTGGTCATATCAACCACTCCCTCTTCTGGAAGAACC
                                 AGGAGGCTACCCTCTGAAGGACCTCTCA
                                                                                                                 302 AGGATGCCATCGACTTGGCTCGCTCGATAGCTCAAGAAGGAATTCAATGCTG
                                                                                                                                                                                                           485 AGCTGGAAGTCACCACGACCGCCAACCAGGACCCTCTGCTTACTCATCATCATCG
                                                                                                                                                                                                                                                                                                                                   TCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCGATTGCAGGCTGCTC
                                                        365 AGAAGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTG
                                                                                                                                                                                                                                                                       GAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGACTATC
                                                                                                                                                                                                                                                                                                  GIGICGATATCTGGGAGCACGCTTTCTACCTCCAATACCTCAACGTCAAGGTTGATTACC
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Pred. No. 5.1e-48;
0; Mismatches 206; Indels
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/organism="unknown"
/mol_type="mRNA"
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Unclassified.
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PYEYNALEPFISADIMWVHHGKHQTYVNNINASTRAYNDAVQAQDVLKQMEILTAVK
FRGGEHVNHALFWKTNAPQSQGGQLNDGPLKQAIDKEFGDFEKFKAAFTAKALGIQG
SGWCWLGLSKTGSLDLVVAKDQPTLTTHHPIIGWDGWEHAWYLQYKNDKASYLKQWWN
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Hallewell, R.A., Mullenbach, G.T., Stempien, M.M. and Bell, G.I. Sequence of a cDNA coding for mouse manganese superoxide dismutase Nucleic Acids Res. 14 (23), 9539 (1986)
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Submitted (25-FBB-2003) Andersson A., Department of Medicine,
Karolinska hospital, Unit of Clinical Allergy Research L2:04, 17176
Stockholm, SWEDEN
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Cloning, expression and characterisation of two new IgE binding proteins in the yeast Malassezia sympodialis with sequence similarities to heat shock proteins and manganese superoxide
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Exobasidiomycetidae; Malasseziales; Malassezia.
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Andersson, A.
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/trānslation="MLCRAACSTGRRLGPVAGAAGSRHKHSLPDLPYDYGALBEPHINA
QMQLHHSRAYNNLINATEBKYHRALAKODYTQVALQPALKRHOGGHINHTIFW
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IAACSNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINNENYTERYT
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Sun,Y., Hegamyer,G. and Colburn,N.H.
Sequence of manganese superoxide dismutase-encoding cDNAs from multiple mouse organs
Gene 131 (2), 301-302 (1993)
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Submitted (25-NOV-1992) Sun Y., FCRDC, CBS, LVC, P.O. Box
Frederick, MD, 21702-1201
Location/Qualifiers
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0; Mismatches 195; Indels
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/citation=[1]
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al Similarity 63.3%;
368; Conservative
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                             452 IGHGGGAGTICAAGGTICAGGCTGGGGTTGGCTTGGCTTCAATAAGGAGCAAGGTCGCTT
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CF638868 D08_A03 F
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CF643783 K12_E10 F
CF643817 K13_A05 F
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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TA ST	4 bp mRNA linear Diploid Ustilago maydis cota; Ustilaginomycetes. ginales; Ustilaginaceae, Saville, B.J. lago maydis Diploid Fillalyses M. Mississauga, ON, L5L.: Mississauga, OS, L5L.: Mr Tow: 03 column: A GAGTAATACGACTCACTATAGGG
CF643863 CA765001 CD4891002 CD271903 CF475965 CF643518 BI904486 CF593893 BU0060841 CD060841 CD060841 CD060841 CD060841 CD060841 CD060841 CD060841 CD060841 CD060841 CD0298030 CA321590 BI412406 CA321590 BI412406 CA321590 BI412406 CA321590 BI412406 CA321590 BI412406 CA321590 BI412406 CA321590 CA321323 CCB668028	CF638868 D08_A03 Filamentous Forced Diploid Ust sequence. CF638868.1 CF638868.1 GF638868.1 GF638868.1 GF638868.1 Ustilago maydis Ustilago maydis Ustilaginomycetidae; Ustilaginales; Ustilaginomycetidae; Ustilaginomycetidae; Ustilaginales; Ustilaginomycetidae; Ustilaginales; Ustilaginal
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Ustilago maydis
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                                                            /db xref="caxon:5270"
/cell type="Mycelia"
/dev_stege="filamentous diploid"
/dolone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
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                                                                                                                                                                                                                                                   CGATGCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCA 167
                                                                                                                                                                                                                                                                                                                                                                                                               287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 CTCTGAAGGACCTCTCAAGAAGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGATGTGCTTACCCAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACATTCCTATCATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 GCACCACCCATCATCGGTGTCGACGCTTGGGAGCACGCTTTCTACCTCCAGTACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTCAAGCCTGACTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGC
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                                                                                                                                                                                                                             Gape
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                                                                                                                                                                                                  DB 14; Length 754;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                              42.7%; Score 285.8; DB 14; ilarity 66.5%; Pred. No. 1.4e-66; Conservative 0; Mismatches 207;
                        organism="Ustilago maydis"
Location/Qualifiers
                                   /mol_type="mRNA"
/strain="FBD12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664
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CF644174 656 bp mRNA linear EST 02-OCT-2003 K17 G06 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA sequence.

GI:37413160

CF644174 CF644174.1

ACCESSION VERSION KEYWORDS SOURCE

DEFINITION

Ustilago maydis

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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

Ustilaginomyceridae; Ustilaginales; Ustilaginaceae; Ustilago.

Ustilaginomyceridae; Ustilaginales; Ustilaginaceae; Ustilago.

E 1 (bases 1.cofs6)

Nugent, K.G., Choffe, K. and Saville, B.J.

Gene Expression during Ustilago maydis Diploid Filamentous Growth:

EST Library Creation and Analyses

Unpublished (2003)

Contact: Barry J. Saville

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Tel: 905 569 4702

Fax: 905 828 3792

Fax: 905 828 3792
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/db_xref="caxon:5270"
/cell type="Mycelia"
/cell type="Mycelia"
/clone lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
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Pred. No. 3.1e-66;
0; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
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CF643817 702 bp mRNA linear EST 02-OCT-2003 K13_A05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
         479 CIAAGAAGCIGGAAGICACCACGACGCCAACCAGGACCCICIGCITACICACAITCCIA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 ACTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCGGATTGCAGG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 702)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene Expression during Ustilago maydis Diploid Filamentous Growth:
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/dev_stage="Mycelia"
/dev_stage="Mycelia"
/dev_stage="Filamentous diploid"
/dev_stage="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPOMT plasmid, with the u
of the Superscript II cDNA Library Construction Kit."
                                                                                                                               cerricaadeadeacercaacercaacrirideerceaceacercaacercaaarecacerrea
                                                                                                                                                                                                                                                                                                                                                                474 ACTCGAAGCTTGAGGTTGTCACCACCAAGGACCAGGACCCTCTGATCTCGCACCACCCA
                                                                         CTCTCAAGAAGGCTATCGAAGGAATCTTTTGGTTCTTTTCGAGGCCTTCAAGAAGAAGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTG
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Ustilago maydis
Bukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
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3359 Mississauga Road North, Mississauga, ON, L5L 1C6,
Tel: 905 569 4702
Fax: 905 838 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D128/9-013-UTM row: 05 column: A
Seq primer: T7 Reverse (5' GACTAATACGACTCACTATACGG 3')
High quality sequence stop: 702.
Location/Qualifiers
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/mol_type="mRNA"
/strain="FBD12"
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Contact: Barry J. Saville
Saville Lab
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Gene Expression during Ustilago maydis Diploid Filamentous Growth:
EST Library Creation and Analyses
Unpublished (2003)
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Tel: 905 569 4702
Fax: 905 828 3792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D128/9-012-UTM row: 10 column: E
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
High quality sequence stop: 662.
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Oryza sativa (indica cultivar-group) cDNA clone C0001833 5' similar
to Superoxide dismutase [Mn], mitochondrial precursor (EC
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                /cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/dev_stage="Filamentous Forced Diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II oDNA Library Construction Kit."
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Pred. No. 1.6e-61;
0; Mismatches 195; Indels
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1 (Dases I to 617)
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3359 Mississauga Road North, Mississauga, ON, LSL 1C6,
Tel: 905 569 4702
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High quality sequence stop: 617.
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/mol_type="mRNA"
/strain="PBI/PB2"
/db_xref="taxon:5270"
/db_type="Teliospore"
/dev_grage="Germinating teliospore"
/dev_grage="Germinating teliospore"
/lobe lib="reliospore"
/note="Vector: pDNR-LIB; Site_1: SfilA; Site_2: SfilB;
mNA was extracted from graminating teliospores. ODNA was
amplified by PCR and unidirectionally cloned into pDNR-LIB
plasmid with the use of Clontech's Creator SMART CDNA
                                                                                                                                                                                                                                                                                                     29-AUG-2003
          TTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAAACGTCAAGCCCTGACTATCTCG 607
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                                                      642 TCGACATCTGNNAACACGCNTTCTACTTGCAGTACAAGAATGTCAAGGCTGACTACCTCA 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sacadura, N.T. and Saville, B.J. Gene expression and EST analyses of Ustilago maydis germinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTCTAGACAGACTTTCGTCGCTCCTGCTTTTCCAGATCAGGGCAAAGCATACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
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                                                                                                                                                                                                                                                                                                  CD489102
T18_F10 Teliospore Ustilago maydis cDNA 5', mRNA sequence.
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                                                                                                                                                         702 AGGCCATCTGGAACGTNATCAACTTTGAAAANATCGANAAGCGCTTTNAAG
                                                                                                                608 CTGCTGTTTGGTCCGTTATCAACTACAAGGGGCCAGAGGCCCCGATTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungal Genet. Biol. 40 (1), 47-64 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Barry J. Saville
                                                                                                                                                                                                                                                                                                                                                                            CD489102.1 GI:34331609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 634)
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/clone_lib="IRRI Drought Stress Panicle Library"
/clone_lib="IRRI Drought Stress Panicle Library"
/note="Vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 NGAAGGAGATCATGACGCTCCACCACCAAGCACCACCAGACCTACGTCAATGGCCTCA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCGCCGAAGAGCCCCCGCCAAGTTTCAACAGTCGGGCGACGTCAAGGCGCAGATCA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 ATTTGCAGGCCGCGTTGAAGTTTAACGGNGGTGGNCACTTGAACCACTCGCTCTTCTGGC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 GCAACCTCGCGCCGACCGACTCGGNCGCTACCAAGCCCGAAGCCGCTCCGACCTTTATCA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 CCGCTGCTGTCCAAGGATCCGGATGGGGCTGGCTTGGACCCGGCTTACTAAGAAGC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOGGACAGCACACCTGCCTGAGCTTCCGTACGCCTATGATGCGCTCGAGCCGTCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCTGCCGAGGAGAGCTACTCGCCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 AGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGAC---CTCTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   S. Rudd of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR64"
/db_xref="taxon:39946"
/clone="C0001833"
                                                                                                                                                                 gi:25994256
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Ehrhartoideae; Oryzeae; Oryza.

1 (baees 1 to 776)

Bennett,J., Aruwqam,K., Lafitte,R., Wen,J., Rudd,S.
Bruskiewich,R.W.

IRRI Drought Stress Panicle cDNA Library
Unpublished (2002)
On Doc 2, 2002 this sequence version replaced gi:2599
Contact: Richard Bruskiewich
Biometrics and Bioinformatics Unit
International Rice Research Institute
                                                                                                                                                                                                                                                                                                                                        Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS;
http://www.iris.irri.org; b0201832
Assignment of putative function to the sequence by
Munich Information Center for Protein Sequences
(http://mips.gsf.ds
                                                                                                                                                                                                                                                                    DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Panicles"
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Les 385; Conserv
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Matches
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JOURNAL
                                                         AUTHORS
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Axenic plate culture") and a third library represents axenically grown plants ('FHIG:C') Axenic plate culture'). Libraries were analyzed in parallel and 3555 (FHIG:A), 3964 (FHIG:B), and 2532 (FHIG:C) high-quality (PHRED 20) ESTS of >99bp have been deposited. The CDNA libraries were constructed from total RNA using the SMART CDNA library Construction kit (#K1051-1, Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. Full-length CDNAs were trimmed by Sfii, fractionated and directionally ligated into (lambda)TriplEx2 arms. The lambda library was converted to a plasmid library via site-specific recombination at loxP sites in a Cre+ strain (E. coli BM25.8). Plasmid clones were randomly collected and analysed by DNA sequencing using a plasmid-specific forward primer (P104).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF472965 TADS1_12_E11.gl_A015 Drought-stressed loblolly pine roots DS1 Pinus taeda_cDNA clone RTDS1_12_E11_A015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TCTCAAGAAGGCTATCGAAGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 carcedraricaraterreseaseacecerriciaecrecaracereaacereaaserre 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 IGCIGCIGCCATCCAGGGCTCTGGCTGGGGCGGCTGGCTTGAACCCCTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 gcadcadarcardacderreaceacadadeacaccacacaacerargereaceacacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GCCCCTCAAGTCAGTTACGC-----GAAACTGCTACTCCCAAGGAGCGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 CCTCCAAGCTGCCCTCCGCTTCAACGGTGGTGTCATATCAACCACTCCCTCTTCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGGAGGCTACCCTCTCTGAAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 GAACCTTGCACCTGCTGCTAGCGAGGGCAAGGGCAAGGGTGGAGAGCTCAAACCTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 ATTGAAGGATGCCATCGACTCGAACTTTGGCTCGCTCGATAGCCTCAAGAAGGAATTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 TAAGAAGCIGGAAGICACCACGACGCCAACCAGGACCCICTGCTTACTCACATTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 caaacgretrgagaregecaccacrecraaccagaccereregagecacarrecear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 GGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCATCTC
      represents axenically grown fungus ('(FHIG:B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 215.6; DB 14; Length 606;
Pred. No. 1.6e-47;
0; Mismatches 179; Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACTTGGCTCCCTATGGATCCG-----
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Best Local Similarity 65.1%;
Matches 376; Conservative
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/strain="ATCC200175(P.involutus);Skuleskogen,Skogsforsk,Sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 01-SEP-2003
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Transcriptional responses of Paxilius involutus and Betula pendula during formation of ectomycorrhizal root tissue
Unpublished (2003)
Contact: Johansson, T.
CAACCAGGACCCTCTGCTTACTCACATTCCTAT-CATCGGAGTTGACATCTGGGAGCACG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Betula pendula/Paxillus involutus mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558 CAACCAGGACCCTCTGCTCTCGCATGGGCCTCTGNATCGGGGTCGACGCTTGGGAACATG
                                                                                                                                                                     AAGAATGGCGGTGAGTTGAGCAGCGCCTCTCAAGGACGCTATCGACCGAGACTTT
                                                                                                                                                                                                                                             GGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACACCCGCTGCTGTCCAAGG-ATC
                                                                                                                                                                                                                                                                                                        gengentriegaceceaecteaagnecaagneaargereaganegereecareeagenrie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD271903 606 bp mRNA linear EST 01-
T143A01367F (FHIG:A) Ectomycorrhiza plate culture Betula
pendula/Paxillus involutus mixed EST library cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lund, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betula pendula/Paxillus involutus mixed EST library
Betula pendula/Paxillus involutus mixed EST library
Eukaryota; mixed EST libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungal-Host Interaction Group (FHIG)
Microbial Ecology, Institution of Ecology
Ecology Building, Lund University, SE-223 62
Fax: +46 46 222 41 58
Email: tomas.johansson@mbioekol.lu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: P104 (5'-GGGAAGCGCCCATTGTGTT-3')
BACKWARD: P105 (5'-AGTGAGCTCGAATTGCGGCC-3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: P104
High quality sequence stop: 606.
Location/Qualifiers
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CF643518 619 bp mRNA linear EST 02-OCT-2003
D91_E07 Filamentous Forced Diploid Ustilago maydis CDNA 3', mRNA
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/note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
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                                                                                                                                            482
                                                                                                                                                                                                    619
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Nugent, K. G., Choffe, K. and Saville, B. J.
Nugent, K. G., Choffe, K. and Saville, B. J.
EST Library Creation and Analyses
Unpublished (2003)
                                                                                                                                                                                                                                                        483 AGCACGCCTTCTACCTCCAGTACCTCAACGTTAAGGCTGATTACCTCGAGGCTATCTGGA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
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  363 AGGGGTCTGGCTGGTGCTGGCTCGGGTTGAACCCCGTCACCAAGCGCTTGGAGATCACCA
                                                                                                                                                                                                 560 AGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGACTATCTCGCTGCTGTTTGGT
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                                                                                                                                            423 ccaccccraarcaggarccrcrcrrrgaarrrgarcccgarcarcaggcgrcgacargragg
                                                                                       CGACCGCCAACCAGGACCCTCTGCTTACTCACATTCCTATCATCGGAGTTGACATCTGGG
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Ustilaginomycetidae, Ustilaginales; Ustilaginaceae; Ustilago.
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3359 Mississauga Road North, Mississauga, ON, L5L 1C6, 0
781: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
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65.3%; Pred. No. 1.2e-46;
Live 0; Mismatches 166; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="FBD12"
/strain="FBD12"
/db_xxef="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: UTM-UM-D126/7-091-UTM row: 07
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   620 CCGTTATCAACTACAAGGAGCAGA 644
                                                                                                                                                                                                                                                                                                                                                                     543 acgrearchachegeaddadgenda 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Barry J. Saville
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Ustilago maydis
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/strain="CCOMES"
/db_xref="taxon:3352"
/db_xref="taxon:3352"
/db_net="RHIOB-T1 plage-resistant E. coli"
/lab_host="DhiOB-T1 plage-resistant E. coli"
/clone_lib="Drought-stressed loblolly pine roots DS1"
/note="Vector: pSill80; Site 1: ECORI, Site 2: XhoI; The
library was prepared from poly4+ RNA from drought-stressed
loblolly pine (Pinus taeda) roots. Water was withheld from
ramet clones until predawn needle water potential reached
1.75 MPa. On day 7 roots were harvested for RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into pSill80. Inserts excised with ECORI
(5' end) and XhoI (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory of Georgias and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: JENREV (CAGGAAACAGCTATGACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AAGGATCCGGATGGGGCTGGCTTGAACCCGCTTACTAAGAAGCTGGAAGTCACCA 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATGACCCTTCACCACCAAGCACCATCAGACTTATGTTAACGGCCTCAACGCTGCCG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 crectrigaaarrcaaceeeegeecacarraaccacrectrerrerresaaaaaaaacrree 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATGGAGCTTCACCACAAGAAGCATCATCAGACCTATGTCAACGCCCTAAACGAAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 AGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGTTAAGCTTCAGT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CCAATGCTTACTCCAGTGCTACATCAGCAAAAAGCGAATCGCC------CTCCAAG 182
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                            An EST database from drought-stressed loblolly pine (Pinus taeda)
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                             Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J.,
Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J.
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                                                                                                                                                                                                                                    Unpublished (2003)
Other_ESTS: RTDS1_12_E11.b1_A015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pinus taeda"
                                                                                                                                                                                                                                                                                              Contact: Cordonnier-Fratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
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                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                           Neale, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim:
Matches 355;
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11647 row: f column: 04
High quality sequence stop: 724.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 730)
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                                                                                                                              CTGGAAGTCACCACGACCCCAACCAACCATCTCCTTACTCACATTCCTATCATCGGA
                                        199 cáddeceredaacerentrificeredecenteaacereaarecaecricaaederaee
                                                                     ACCGCTGCTGTCCAAGGATCCGGATGGGGCTGGCTTGAACCCCGCTTAAGAAG
                                                                                                  ATTGCCACCATCCAGGGCTCTGGTTGGGGCTGGCTTGGTTTCAACCCCAAGAACTCGAAG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                  607 GCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGCAGAGGCCCGATTGCAGGCTGCTC
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/strain="Czech II"
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Mus musculus
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DB 12; Length 730;

Score 212.2;

31.7%;

Query Match

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 995)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 PL607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
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                                 Indels
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Pred. No. 1.5e-46;
0; Mismatches 193;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. [ bases 1 to 746]
Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C. Analysis of expressed sequence tags from Gibberella zeae (anamorph
                                                                                                                         Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
                                                                                                                                                                                                                                                                                                                   column: 18
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                             Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
                                                                                                                                                                                            Contact: Frances Trail
Department of Plant Biology
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Plate: 1 row: K co
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Matches 351; Conservative
                Gibberella zeae
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/note="Organ: pancress; Vector: pSPORTI; Site 1: Sall;
Site_2: Not1; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
islets 1 MS1-A, and Kaesther ngg1 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCCTTACCCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 CICCAAGGAGAICAIGACCTITCACCACCAAGCACCAICAGACTIAIGITAACGGCCI
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                       31.5%; Score 211; DB 14; Length 995; 63.2%; Pred. No. 3.9e-46; ive 0; Mismatches 195; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 GACAAACCTGAGCCCTAAGGGTGGTGGAGAACCCA-
     column: 07
                                                                                            organism="Mus musculus"
                  High quality sequence start: 21
High quality sequence stop: 522.
Location/qualiflers
1..995
                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                            /clone="IMAGE:6431706"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
       Plate: IRBD19
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Matches 366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGA 367
                                                                                            /db_xref="taxon:5518"
/clone lib="Carbon-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCTGCTGTCCCAAGGATCCGGATGGGGCTGGCTTGGCTTGAACCCGGCTTACTAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCCGGTATCCAGGCTCCGGCTGGGCTCGTCCAGGACAAGAACGCTGGCACTC
                                                                                                                                                                                                                                                                                                                                                             126 TCCGCGCCAAGGCCACTCTCCCCAACGACTATGGCGCTCTTGAGCCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                   128 TCTCCAAGGAGATCATGACCCTTCACCACCAAGCACCATCAGACTTATGTTAACGGCC
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                                                                                                                                                                                                                     Length 746;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                     31.5%; Score 210.8; DB 13;
61.9%; Pred. No. 3.7e-46;
iive 0; Mismatches 213; 1
                         zeae"
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1. .746
/organism="Gibberella
/mol_type="mRNA"
/strain="NRRL 31084"
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EST 26-AUG-2002

746 bp mRNA linear BST 26-AUG-2 Carbon-starved mycelia Gibberella zeae cDNA, mRNA

BU060841.1 GI:22501130

Fgr-C_1_K18_T3 sequence.

DEFINITION

ACCESSION VERSION KEYWORDS

BU060841

linear

497 506 557

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AT002967 AT002967 POSLM01 Pleurotus ostreatus CDNA clone 460LM, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Fungi; Basidiomycota, Hymenomycetes, Homobasidiomycetes, Agaricales; Pleurotaceae; Pleurotus.

1 (bases 1 to 468)
Lee, S.H., Kim, B.G., Kim. K.J., Lee, J.S., Yun, D.W., Hahn, J.H., Kim, G.H., Lee, K.H., Sub, D.S., Kwon, S.T., Lee, C.S. and Yoo, Y.B. Comparative Analysis of Sequences Expressed during the Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ddaadarrrcaadaaaaagrrcaacacaaccacrecre-rerccaaggcagregcregge 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="shaking liquid cultured mycelia"
/lab_host="E.coli"
/clone lib="POSIMO1"
/note="Vector: lambda Uni-ZAP XR; Site 1: EcoRI; Site 2:
XhoI; average insert size:1000 bp;initial pfu:5 X 10 7
Library information:Isolation of total RNA from the
mycelia incubated in shaking liquid MCM media at 30 deg 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Division of applied microbiology Sational Institute of Agricultural Science and Technology (NIAST) Seodundong, Suwon, Kyung-gi 441-707, South Korea Email: bgkim@niast.go.kr
498 NGGTTGGGGNTGGCTCGGCTACAACCCGCAGAAGCTCGACATNGTCACTACCGC
                                                                 -GGATGGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCTGGAAGTCACCACGACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bgkim@niast.go.kr
Submitted through BRIC(Biological Research Information Center)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 209.6; DB 9;
Pred. No. 6e-46;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. Biol. 35 (2), 115-134 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .468
/organism="Pleurotus ostreatus"
                                                                                                                                                                                                                                                                                                                                                                                                                     Pleurotus ostreatus (oyster mushroom)
Pleurotus ostreatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        URL: http://bric.postech.ac.kr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="ASI 2029"
/db_xref="taxon:5322"
/clone="460LM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cocation/Qualifiers
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72.9%;
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                                                                                                                                                                                                                                                                                                             DEFINITION
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Matches
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MEDLINE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="reliospore"
/note="Vector: pDNR-LIB; Site_1: SfilA; Site_2: SfilB;
note="Wector: pDNR-LIB; Site_1: SfilA; Site_2: SfilB;
mNRA was extracted from germinating teliospores. cDNA was
amplified by PCR and unidirectionally cloned into pDNR-LIB
plasmid, with the use of Clontech's Creator SMART cDNA
Library Construction Kit."
                                                            EST 29-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTICAACGGAGGACACATCAATCACTCTCTGTTCTGGAAGAACTTGGCTCCCTAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AACTTTAACGGCGGTGGTCACATCAACCACTCTCTTTTGGGAGAATCTGGCCCCGCAG 377
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                                                                                                                                                         Ustilago maydis
Ustilago maydis
Bukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
1 (bases 1 to 577)
Sacadura, N. T. and Sav<u>il</u>le, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bsaville@utm.utoronto.ca
Seg primer: M13 reverse primer (5' AAACAGCTATGACCATGTTCA 3').
Location/Qualifiers
                                                        l
Teliospore Ustilago maydis CDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     3359 Mississauga Road North, Mississauga, ON,
Tel: 905 569 4702
Fax: 905 828 3792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5270"
/cell_type="Teliosspore"
/dev_stage="Germinating teliospore"
/lab_host="E. coll"
                                                                                                                                                                                                                                                                                                                                Genet. Biol. 40 (1), 47-64 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210.4; DB 1
Pred. No. 4.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Ustilago maydis"
                                                                                                                                                                                                                                                                                     Gene expression and EST analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'mol_type="mRNA"
'strain="FB1/FB2"
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                                                                              T03_D04 Teliospore Ustil
CD488011
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Search completed: April 1, 2004, 21:52:38 Job time : 1732 secs

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Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 29, Appl
Sequence 1627, Ap
Sequence 90403, A
Sequence 91503, A
Sequence 1822, App
Sequence 1823, App
Sequence 1820, App
Sequence 1905, App
                                                                                                                           April 1, 2004, 12:34:16; Search time 233.318 Seconds (without alignments) 10723.022 Million cell updates/sec
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'(gnn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
'(gnn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
'(gnn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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'(gnn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-109-670-3
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US-09-917-800A-1627
US-10-424-599-90405
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Sequence 122, App	Sequence 22, Appl	Sequence 294, App	Sequence 709, App	Sequence 9, Appli	Sequence 1, Appli	Sequence 25, Appl	Sequence 1, Appli	Sequence 182, App	Sequence 1, Appli	Sequence 3227, Ap	Sequence 1, Appli	Sequence 5397, Ap	Sequence 1, Appli	Sequence 14744, A	Sequence 16177, A	Sequence 8, Appli	Sequence 24298, A	Sequence 11, Appl	Sequence 4975, Ap	Sequence 13978, A	Sequence 731, App	1397	Sequence 14457, A			67, 7	Sequence 45520, A	Sequence 5724, Ap	12085,
14 US-10-247-671-122	10 US-09-971-429B-22	15 US-10-310-154-294		14 US-10-230-331-9	9 US-09-727-855B-1	14 US-10-109-670-25	9 US-09-818-564-1	10 US-09-911-904-182	3 15 US-10-289-762-1	9 US-09-738-626-3227) 9 US-09-738-626-1	14 US-10-156-761-5397	14 US-10-156-761-1	9 US-09-960-352-14744	10 US-09-918-995-16177	9 US-09-987-190-8	10 US-09-918-995-24298	9 US-09-993-333-11	9 US-09-960-352-4975		9 US-09-960-352-731	9 US-09-960-352-13976	_	_	9 US-09-960-352-5493	_	12 US-10-424-599-45520	9 US-09-960-352-5724	9 US-09-960-352-12085
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27.7	27.6	27.2	26.6	25.5	22.6	21.2	20.8	20.3	20.1	19.9	19.9	19.0	19.0	18.4	17.3	16.7	16.6	16.0	15.8	15.7	15.3	15.1	15.0	14.7	14.6	14.0	13.8	13.5	13.5
185.4	184.6	182.2	178	170.8	151.4	142	139	136	134.6	133.4	133.4	127	127	123.4	116	111.4	111	107	106	104.8	102.6	100.8	100.4	98.6	98	93.8	92.4	90.6	90.6
16	17	18	19	20	21	22	23	24	25	26	27	78	c 29	30	31	32	33	34	35	36	37	c 38	39	c 40	c 41	42	43	c 44	c 45

ALIGNMENTS

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Sequence 4, Application US/09727855B
Patent No. US20020168703A1
GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: STGOTICHI, Yutaka
TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUI
TITLE OF INVENTION: MATERIALS THERROF
FILE REFERRNCE: C38435/111694
CURRENT FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARES PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 669
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ORGANISM: Phaffia rhodozyma
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OTHER INFORMATION: n or X
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ION: (1). Total
INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
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               TCTAAGGAAATCATGATCCTTCACCACTCCAAGCACCATCAGACTTACGTCACCAACCTC
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TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
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Pred. No. 1.2e-73;
0; Mismatches 200; Indels
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CURRENT APPLICATION NUMBER: US/10/109,670
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 3
LENGTH: 728
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al Similarity 65.5%;
385; Conservative (
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ORGANISM: Malassezia furfur
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US-10-109-670-3
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APPLICANT: OJIMA, Kazuyuki
APPLICANT: OJIMA, Kazuyuki
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY
TITLE OF INVENTION: MATERIALS THERROF
FILE REFERENCE: C38435/111694
CURRENT APPLICATION NUMBER: US/09/727,855B
CURRENT FILING DATE: 2000-12-01
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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301 CIGITCIGGAAGAACTIGGCTCCCTAIGGAICCGAGGAGGCTACCCTCTGTGAAGAACCT
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llarity 72.0%; Pred. No. 2.5e-95;
Conservative 0; Mismatches 159;
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OTHER INFORMATION:
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LOCATION: (1)
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US-09-727-855B-6
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LENGTH: 597
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LOCATION: (1). [(630)
OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
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Publication No. US20030105283A1
GENERAL INFORMATION:
APPLICANT: TRESAKO, KAZUTOH et al.
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
FILE REFERENCE: 1422-0523P
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Local Similarity 62.5%; Pred. No. 3.7e-63;
les 343; Conservative 0; Mismatches 206;
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ORGANISM: Malassezia furfur
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US-10-109-670-29
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: OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
US-10-109-670-4
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                                                     188 TCCAGCTGCAGAGTGCGATCAAGTTCAACGCGGGGGCCACATCAACCACTCGCTGTTCT
                                                                                                                                         GGAAGAACCTGGCCCCCCAGAGCGAGGTGGTGGCCAACTGAACGATGGCCCTCTCAAGC
                  GGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGA
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Publication No. US20030105263A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
CURRENT APPLICATION NUMBER: US/10/109,670
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 58
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Best Local Similarity 63.9%; Pred. No. 3.6e-73;
Matches 379; Conservative 0; Mismatches 214;
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ORGANISM: Malassezia furfur
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NAME/KEY: misc_feature
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LENGTH: 812
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Sequence 90405, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
CEO YOUNGWE!
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: VOMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                  GAAGAACTIGGCICCCIAIGGAICCGAGGAGGCIACCCICTCIGAAGGACCICTCAAGAA 368
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Pred. No. 4e-57;
0; Mismatches 212; Indels
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Best_Local Similarity 61.1%;
Matches 352; Conservative (
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                          421 CTGATTGGCATCGATGCGTGGGAGCACGCGTACTACCTGCAGTACAAGAACGTCAAGGCC 480
                                                                                                                                                                                                                                                         GACTACTTCAAGGCGATCTGGACCGTGATCAACTTTGAGGAGGCCGAGAAGCGTCTCANG 540
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                                                                                                                                                                                                     GACTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGGGCAGAGGCCCGATTGCAG
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US-09-917-800A-1627
  18;
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Pred. No. 8.6e-58;
0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CASSIE, ANCHAE

APPLICANT: Gassie, Anchae

APPLICANT: Gane Logic, Inc.

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5038-US

CURRENT APPLICATION NUMBER: US/09/917,800A

CURRENT FILING DATE: 2001-07-31

PRIOR PELICATION NUMBER: US 60/222,040

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR APPLICATION NUMBER: US 60/290,029

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-15

PRIOR FILING DATE: 2001-05-15

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-16

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/297,457

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-19

PRIOR PLING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1627, Application US/09917800A Patent No. US20020119462A1
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Best Local Similarity 62.5%;
Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Mendrick, Donna
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES DIFFERENCE: PA 0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGram
                                                    1441 CACACATTTTGGCTCTTTTGAAGCATTAGTACAAAAGTTAATGCAGAAGGTGCTGCACT 1500
                                                                                                                                                            1501 Acadedercredardedereredecrredakeaagageredadageerreraginga 1560
                                                                                                                                                                                                                                                                                                                                                                                         1621 TATTGATGTTTGGGAGCATGCGTACTACTTACAGTACAAGAATGTTAGACCAGACTATCT 1680
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437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 TAAGCTITCAGTCTGCTCTCAAGTICAACGGAGGAGGACACATCAAICACTCTCTGTTCTG 308
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378 GGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACACCGCTGCTGT
                                                                                                                                                                                                                                                                           1561 AACCACTGCCAACCAGGACCCACTGGTTACTAAGGGACCAAATTTGGTTCCATTGCTTGG
                                                                                                           438 CCAAGGAICCGGAIGGGCTGGCTTGGCTTGAACCCGCTTAAGAAGAAGCTGGAAGTCAC
                                                                                                                                                                                                                      ---CATTCCTATCATCGG
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                                                                                                                                                                                                                                                                                                                                     546 AGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGACTATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT
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Pred. No. 1.9e-55;
0; Mismatches 217; Indels
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 010001CB1
US-10-044-090-836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1681 GAAGAACATTTGGAAAGTTATTTAATTGGAAATATGC 1716
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Best Local Similarity 60.9%;
Matches 366; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                          377
                                                                                                                                                                                                                                              438 CCAAGGATCCGGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCTGGAAGTCAC 497
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                       318 GGCTCCCTATGGATCCGAGGCTACCCTCTCTGAAGGACCTCTCAAGAGGCTATCGA
                                                                           566 AGCTCCTGTTCGTGAAGGAGGTGGTGAACCACCCAAGGGTTCACTGGGATGGGCTATTGA
                                                                                                                                  378 GGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACACGCTGCTGT
                                                                                                                                                                                      506 CACACATTTTGGTTCTTTTGAAGCATTAATACAAAAGTTAACGCAGAAGGTGCTGCACT
                                                                                                                                                                                                                                                                                                     446 ACAGGGGTCTGGATGGGTGTGGCTTGGACAAAGAGTTGAAGAGGCTTGTAGTTGA
                                                                                                                                                                                                                                                                                                                                                            CACGACCGCCAACCAGGACCCTCTGCTTACTCA-------CATTCCTATCATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 2217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT MRT3847 52646C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 TAAGAACATTIGGAAAGITATTAATIGGAAATAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 90403, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-10-424-599-90403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-90403
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LENGTH: 2217
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190 GAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCAAGGGAGATGTTACAGCCCAGAT
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CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1822, Application US/09954456 Patent No. US20220115057A1 GENERAL INFORMATION:
APPLICANT: Young, Paul
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larity 60.9%;
Conservative
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LENGTH: 1026
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 6/306,220
PRIOR APPLICATION NUMBER: 6/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FSESSEQ for Windows Version 4.0
SEQ ID NO 13503
LENGTH: 996
                                                                                                       69 CAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT
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-CACATTCCTAT
                                    570 ACAAATTGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAGGCCTTATTCCACT
                                                                             CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGTCAAGCCTGA
                                                                                                                                                        CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGGGGCAGAGGCCCGATTGCAGGC
                                                                                                                                                                                             690 TTATCTAAAAGCTATTTGGAATGTAATCAACTGGGAGAATGTAACTGAAAGATACATGGC
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489 GGAAGTCACCACGACCGCCAACCAGGACCCTCTGCTTACT-
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US-10-198-846-13503
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
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507 IGTIGGIGICCAAGGCICAGGIIGGGGIIGGCIITGGIITICAAIAAGGAACGGGGACACIT 566
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                                                                    CACATTCCTAT
                                                                                                                           ACAAATTGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAAGGCCTTATTCCACT
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Pred. No. 1.9e-55;
0; Mismatches 217;
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APPLICANT: Dai, Hongyue
APPLICANT: Dai, Fudong
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Honsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Nan de Vijeer, Marc J.
APPLICANT: Van de Vijeer, Marc J.
APPLICANT: Salol-188-999
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-04
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 GGAAGTCACCACGACCGCCAACCAGGACCCTCTGC-----TTACTCACATTCCTAT
130 CAACGCGCAGATCATGCAGCTGCACCACGACGACCGCGGGCCTACGTGAACAACCT
                                                                                                                               190 GAACGTCACCGAGGAGGAGTACCAGGAGGCGTTGGCCAAGGGAGATGTTACAGCCCAGAT
                                                                                                                                                                                GAAGAACTIGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA
                                                                                                                                                                                                                                                                                                                               GACAAACCTCAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AGCCATCAAACTGGACTTTGGTTCCTTTGACAAGTTTAAGGAGGAAGCTGACGGCTGCATC
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                                                                                CAACGCTGCCGAGGAGGTACTCGGCCGCTGTGGGCAAGGAGGATGTGCCTTACCCAGGT
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Best Local Similarity 60.9%;
Matches 366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1905, Application US/1
Publication No. US20040058340A1
GENERAL INFORMATION:
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US-10-342-887-1905
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US-10-342-887-1905
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                                                                             APPLICANT: Mao, Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: 10/10/342,887
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
                                                                                                                                                                                                                                 GGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCCTTCAAGAAGAAGTTCAACGCTGACAC
                                 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCTCTCTGAAGGACCTCTCAAGAA
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Pred. No. 1.9e-55;
0; Mismatches 217;
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Bernards, Rene
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Publication No. US20040058340A1
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Best Local Similarity 60.9%;
Matches 366; Conservative
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                                         CAGGGCAAAGCATACCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT
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                                                                                                                      CTCCAAGGAGATCATGACCCTTCACCACACCCAAGCACCATCAGACTTATGTTAACGGCCT
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  Gaps
  18;
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APPLICANT: Medeord, Miliam V.
APPLICANT: Haas, William David
APPLICANT: Haas, William David
APPLICANT: Garles A.
APPLICANT: Slader, Ted
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: thaliana
  Indels
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217;
  Mismatches
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Patent No. US2002023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
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Matthew, Abraham V.
Ledford, Brooke L.
Woesner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
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Raines, Tracy M.
  Conservative
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Nama, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, XITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 50/306,220
PRIOR SEQ ID NOS: 14084
SOFTWARE: FASESEQ FOR Windows Version 4.0
                                                                                                                                 CAACGCGCAGATCATGCTGCTGCACCACAGCAAGCACGCGGCCTACGTGAACAACCT
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                                                      CTCCAAGGAGATCATGACCCTTCACCACACCACCATCAGACTTATGTTAACGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 13787, Application US/10198846; Publication No. US20030099974A1; GENERAL INFORMATION:
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; ORGANISM: HOMO &
US-10-198-846-13787
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LENGTH: 2825
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FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER: OF SEQ ID NOS: 999
SEQ ID NO 745
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Search completed: April 1, 2004, 14:11:04 Job time: 253.318 secs

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GenCore version 5.1.6
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Aar75193 Human man	Aaw98177 Human man	Aar60359 MnSOD N-t	Aap80602 Sequence	Aar75191 Human man	Aar20015 Mn-SOD (I	Aar60360 MHS:MnSOD	Aay55846 Human man	Aay55849 Human man	Aap80603 Seguence		Aag23781 Arabidops	Aag53200 Arabidops	Aar60361 MHS2:MnS0	Abb64067 Drosophil	Aar05542 MnSOD (su	Aar05826 Manganese	Aaw61476 A. fumiga	Aar05825 Manganese	Aar05543 MnSOD (su
AAR75193	AAW98177	AAR60359	AAP80602	AAR75191	AAR20015	AAR60360	AAY55846	AAY55849	AAP80603	AAR75192	AAG23781	AAG53200	AAR60361	ABB64067	AAR05542	AAR05826	AAW61476	AAR05825	AAR05543
7	~	0	Н	N	~	N	m	m	Н	N	e	٣	N	4	~	7	7	7	71
222	222	199	198	198	199	199	198	226	198	198	231	231	199	217	228	228	207	265	265
53.3	53.3	53.1	52.9	52.9	52.8	52.7	52.6	52.6	52.6	٠	52.6	52.6	52.2	52.0	51.3	51.1	50.7	50.3	50.3
614	614	612	610	610	609	608	607	607	909	909	909	909	602	009	592	589		580	280
56	27	28	53		31		33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Antigenic proteins from the fungus Malassezia - bind to IgE antibodies present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.
                                                                                             Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
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                                                                                                                                                                                                                                                Kuroda M,
                                                                             Malassezia fungus MF-4 antigenic protein.
                                                                                                                                                                                                                                               Yagihara T,
Yamaguchi H;
                  Ą
                AAW29771 standard; protein; 224
                                                                                                                                                                           96WO-JP003602.
                                                                                                                                                                                            95JP-00346627.
96JP-00257612.
                                                                                                                                                                                                             96JP-00257613.
                                                                                                                                                                                                                               (TAKI ) TAKARA SHUZO CO LTD
                                                            (first entry)
                                                                                                                                                                                                                                               Okado T,
Yasueda H,
                                                                                                                                                                                                                                                                         WPI; 1997-332788/30.
N-PSDB; AAT85877.
                                                                                                      allergy; antigen
                                                                                                                                                                          10-DEC-1996;
                                                                                                                                        WO9721817-A1
                                                                                                                                                                                             12-DEC-1995;
                                                                                                                                                                                                     05-SEP-1996;
                                                                                                                                                                                                             05-SEP-1996;
                                                                                                                                                                                                                                              Takesako K,
                                                  27-AUG-2003
23-FEB-1998
                                                                                                                                                          19-JUN-1997
                                                                                                                       Malassezia.
                                                                                                                                                                                                                                                         Akiyama K,
                                  AAW29771;
RESULT 1
         AAW29771
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The present sequence represents a specifically claimed antigenic protein isolated from the fungus Malassezia. The antigenic protein can bind to IgE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be wised in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)

Claim 38; Page 85-86; 162pp; Japanese.

Length 206;

47;

202

62

Sequence 224

g

Query Match Local

128;

Matches

67 99

à

gg

187

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or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the reavefor comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides equence which for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a
                                                                                                                                                       VKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNAD 142
                                                                                                                                                                                 123 AAGIQGSGWLWLGVAP-TGNLDLVVAKDQDFLTTHHPVIGWDGWEHAWYLQYKNDKASYL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                    23 IRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQ
                                                                                                                                                                                                                                   TAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDYL
  DB 2;
58.0%; Score 668.5; DB 2 63.1%; Pred. No. 1.7e-63; ive 24; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Protein CAA39937, SEQ ID NO 11539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD45869 standard; protein; 222 AA.
                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765.
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                    Best Local Similarity 63.1
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                AAVWSVINYKEAEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-268312/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER AG.
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                                                                                                                                                           83
                                                                                                                                                                                                                                       143
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  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD45869
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                 1;
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                                                                                                                                                                                                                      The present sequence represents a specifically claimed antigenic protein isolated from the fungus Malassezia. The antigenic protein can bind to IGE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be used in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                           65
                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic proteins from the fungus Malassezia - bind to IgE antibodies present in patients with Malassezia allergies, useful for diagnosis, treatment and prevention of such conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malassezia, fungus, antigenic, human, IgE, immunoglobulin E, antibody;
                                                                                                                                               11 SRQTFVAP----AAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAA
                                                                                                                                                                                                  EESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIE
                                                                                                                                                                                                                                                                             ESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato I;
                                        Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onishi Y,
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                           EHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQAAL 222
                                                                                                                                                                                                                                                                                                                                                                              60.0%; Score 692; DB 2; 59.3%; Pred. No. 5.4e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuroda M,
                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malassezia fungus MF-3 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 36; Page 83-84; 162pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yagihara T, I
Yamaguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29770 standard; protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-JP003602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                   Conservative
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Yasueda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT85876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy; antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 206 AA;
        AA;
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05-SEP-1996;
05-SEP-1996;
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WO9721817-A1

Malassezia.

27-AUG-2003 23-FEB-1998

AAW29770;

AAW29770 RESULT

10-DEC-1996;

Takesako K,

Akiyama K,

19-JUN-1997.

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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent dinot form part of the printed specification, but was obtained in electronic form directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       59 YVNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSE 118
                                                                                                                                                                                                                                                                                                                                    GPLKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---L 175
                                                                                                                                                                                                                                                                                                                                                    58 YVNNLNVTEEKYHEALAKGDVTTQVALQPALKFNGGGHINHSIFWTNLSPKGGGE---PK 114
                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                     1 MLCRAACSAGRR---LGPAASTAGSRHKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAT
                                                                                                                                                                                                                                       1 MSVRASLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQT
                                                                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superoxide dismutase; MnSOD; SOD; human; protein engineering; enzyme engineering; antioxidant; antiinflammatory; cytotoxicity; inflammation; reperfusion injury; therapy.
                                                                                                                                                                                           Length 222;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                 176 THIPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEAR 217
                                                                                                                                                                                                                                                                                                                                                                                               GLIPLLGIDVWEHAYYLQYKUVRPDYLKAIWNVINWENVSQR
                                                                                                                                                                                           DB 7;
                                                                                                                                                                                          Query Match 55.0%; Score 634.5; DB 7; Best Local Similarity 55.4%; Pred. No. 8.7e-60; Matches 123; Conservative 30; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human native manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Gln, Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Gln-143"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Asp-159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW98170 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Tyr-74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tyr-58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "His-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "His-26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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/note= '
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                     Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-1999
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                                                                                                                                                                                           Query Match
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This protein is human manganese superoxide dismutase (hMnSOD). Novel hMnSOD proteins having catalytic activity which differs from this natural hMnSOD are claimed (see AMMS1777). The modified proteins exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the erzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. The modified hMnSOD, or expression vectors in which modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can be used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of the disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKXRAHLQIAACPNQDPLQGTTGLIPL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a human manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant human manganese superoxide dismutase proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.0%; Score 623; DB 2; Length 222; 53.6%; Pred. No. 1.5e-58; tive 31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 53-54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08204 standard; protein; 222 AA
'note= "Trp-161"
                                                                /note= "His-163"
                                                                                                                                                                                                                                                                                         98WO-US018842.
                                                                                                                                                                                                                                                                                                                                                                 97US-00927230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 53.63
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nick HS, Silverman DN
                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-229242/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 222 AA;
                                                                                                                                                                                                                                                                                         10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                              10-SEP-1997;
                                                                                                                                        WO9913088-A1
                                  Active-site
                                                                                                                                                                                                                 18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB08204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB08204
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MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion; injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression plasmid in Escherichia coli host system - encodes human manganese superoxidedismutase analogue, useful for e.g. treating
                                                                                                                                                                                                                                                                                                                                                                                           (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig la-1c; 27pp; English.
                                                                                                                                                                                                                                                                                               85US-00801090.
86US-00907051.
86IE-00002851.
87US-00032734.
89US-00453057.
                                                                                                                                                                                                                                                                      92US-00912213
                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Hartman JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-404931/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ53193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 222 AA;
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                      10-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation
                                                                                                                                                                                                           US5270195-A.
                                                                                                                                                                                                                                                                                                                              29-OCT-1986;
27-MAR-1987;
                                                                                                                                                                                                                                                                                                 22-NOV-1985
12-SEP-1986
                                                                                                                                                                                                                                                                                                                                                              13-DEC-1989
                                          25-MAR-2003
21-JUN-1994
                                                                                                                                                                                                                                        14-DEC-1993
                                                                                       MnSOD cDNA
               AAR44801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                        Beck Y,
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (hAm SÖD). The specification describes a modified hAm SOD which has a catalytic activity which differs from natural hAm SOD in that it exhibits reduced or no product inhibition compared to natural hAm SOD. The natural hAm SOD is especially modified with one or more substitutions in amino acids 26, 30, 34, 74, 143, 159, 161 and 163. The modified hAm SOD is useful for protecting a cell from damage caused by superoxide radicals and for treating a cell from damage caused by superoxide validation and superoxide radicals. The protein is useful for treating inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human manganese superoxide dismutase protein useful as antioxidant for treating cytotoxicity caused by superoxide radicals, inflammation and reperfusion injury following ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents a human manganese superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.0%; Score 623; DB 3; Length 222; 53.6%; Pred. No. 1.5e-58; live 31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Ala encoded by GGA"
                                                                                                                                                 label= Gln, Glu
note= "encoded by CAA"
                                                                           .. .24
'note= "signal peptide"
                                                                                                       5. ,222
note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reperfusion injury following ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 27-28; 27pp; English.
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                      98US-00151052
                                                                                                                                                                                                                                                                                                                97US-00927230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Nick HS;
                                                                                                                                                                                                                                                                                                                                              (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                           2000-578537/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
 reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA63891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 222 AA;
                                                                                                                                    Misc-difference
                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                            Silverman DN,
                                                                                                                                                                                                                                                                                      10-SEP-1998;
                                                                                                                                                                                                                                                                                                                  LO-SEP-1997;
                               Homo sapiens
                                                                                                                                                                                                                          US6107070-A
                                                                                                                                                                                                                                                        22-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                           Peptide
                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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S X S X X B B B B B X B X X B X X B X X B

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NAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AIEESFGSFBAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                               62
The sequence is of a maganese superoxide dismutase which can be used to catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide and molecular oxygen. It can be used to reduce reperfusion injury following ischaemia and prolong the survival of excised organs. It can also me used as a long acting anti-inflamatory drug. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                           SLSSVSRQTFVAPAAFQI---RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                            61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                        53.9%; Score 621; DB 2; 53.6%; Pred. No. 2.5e-58; iive 31; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR90713 standard; protein; 222 AA
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.6%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
AAR90713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΩX
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AAR44801 standard; protein; 222 AA.

RESULT 6 AAR44801 ID AAR

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124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180

g

δ g

181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA

64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123

à 셤 ò

S AVGGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAOIMQLHHSKHHAAAYVNNL 62

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Human, manganese superoxide-dismutase, T-lymphocyte, probe; cDNA,
Escherichia coli, plasmid pMS8-4; N-terminal truncation, cloning,
aminopeptidase, antiinflammatory, oxygen free radical scavenger;
synovial inflammation; arthritis; lung fibrosis.
                                   Human manganese superoxide-dismutase.
                                                                                                                "Pre-peptide"
                                                                                                                                                                                                                                                                                          (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                  iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                         Beck Y, Nimrod A;
                                                                                                                                                                                                                                                                    87US-00032734.
88US-00161117.
                                                                                                                                                                                                                                                      95EP-00106995
                     (first entry)
                                                                                                                                                                               147. .148
                                                                                                                                                                                               sequence"
                                                                                                                       .48
                                                                                                                'note=
               (revised)
                                                                                                                                                                                                                                                                                                                      WPI; 1996-059735/07.
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT15589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 222 AA;
                                                                                                                                                   Misc-difference
                                                                                                                                                                 Misc-difference
                                                                                                                                     Misc-difference
                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                     27-MAR-1987;
                                                                                                                                                                                                                                                      25-MAR-1988;
                                                                                                                                                                                                                                                                            26-FEB-1988;
                                                                                    Homo sapiens
             25-MAR-2003
                     06-APR-1996
                                                                                                                                                                                                                                                                                                         Hartman JR,
                                                                                                                                                                                                                                         10-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   field.)
AAR90713;
                                                                                                         Peptide
                                                                                                                                                                                                     Region
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Human manganese superoxide dismutase (MnSOD) (AAW00018) catalyses the reduction of superoxide radicals to H2O2 and O2. Recombinant MnSOD can be obtd. using transformed host cells, sep. Bscherichia coli cells contg. a plasmid carrying e.g. a cDNA clone (AAT34277) obtd. from a human T-cell library. The MnSOD is useful for reducing reperfusion injury, treating linflammathon or bonochial pulmonary dysplasia and for prolonging survival of excised organs. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of recombinant human manganese super:oxide dismutase - for treating inflammation or bronchial pulmonary dysplasia, reducing reperfusion
                                                                                                                                                                                                                          Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia; bronchial pulmonary dysplasia; inflammation; antiinflammatory.
                                                                                                                                                                                 manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injury or prolonging organ survival.
                                                                                                                                                                                                                                                                                                                                                  1. .24
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                    25. .222
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOT-) BIO-TECHNOLOGY GENERAL CORP
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1A-1C; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86US-00907051.
86IE-00002851.
87US-00032734.
89US-00453057.
92US-00912213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00370461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85US-00801090
                                          AAW00018 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00912213
                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-361912/36.
N-PSDB; AAT34277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1986;
29-OCT-1986;
27-MAR-1987;
13-DEC-1989;
10-JUL-1992;
14-SEP-1993;
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-1995;
                                                                                                                      25-MAR-2003
24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hartman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS5540911-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-1996
                                                                                AAW00018;
                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                        Protein
RESULT 8
AAW00018
                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            generation of oxygen free radicals, particularly synovial inflammation, arthritis and lung fibrosis (claimed). (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a human manganese superoxide-dismutase (MnSOD), and is encoded by a human T-lymphocyte cDNA isolated from a library in phage lambda-gtl0 in Bacherichia coli, by screening with a 5-probe (AATISS91) and a 3'-probe (AATISS92), followed by subcloning in plasmid pBR322 to give plasmid pMS8-4. The cDNA may be expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD product may be cleaved with Aeromonas proteolyvica aminopeptidase to produce an N-terminally truncated analogue with lysine and optionally histidine residues removed. The MnSOD analogue may be used in therapy of conditions associated with generation of oxygen free radicals, particularly synovial inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - having a Lys an for treating e.g.
                                                                                                                                                                                                    /note= "Residues not present in previously published
                                   note= "Region used to construct probe AAT15591"
                                                                                                                                                                                                                                          203. .213
/note= "Region used to construct probe AAT15592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                              note= "Gln in previously published sequence"
                                                                                                                  /note= "Gln in previously published sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.9%; Score 621; DB 2; Length 222; 53.6%; Pred. No. 2.5e-58; Live 31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human manganese super:oxide dismutase analogues opt. His residue absent from the N-terminus, useful synovial inflammation, arthritis or lung fibrosis.
                                                                                                                                                          /note= "Gln in previously published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 118; Conservative
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Best Local Similarity

Query Match

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/note= "His-30"
                                                                                                                                                                                                            Query Match
Best Local Similarity 53.6*
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1999 (first entry)
      WPI; 1999-229242/19.
              N-PSDB; AAX24998
                                                                                                                                                                                              Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW98175;
                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
AAW98175
ð
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                           Db
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                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                        4
                                                                                       64 NAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSBEATLSEGPLKK 123
                                                                                                63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                                                                                       AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                    1.20 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKQRGHLQIAACPNQDPLQGTTGLIPL 179
                                                                       62
                                                                  S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                      6 SLSSVSRQTFVAPAAFQI -- RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                        Gaps
                                                                                                                                                                                                                                                                              Superoxide dismutase; MnSOD; SOD; human; protein engineering; enzyme engineering; antioxidant; antiinflammatory; cytotoxicity; inflammation; reperfusion injury; therapy.
                                       10;
                       Length 222;
                                       61; Indels
                                                                                                                                                      IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                               53.9%; Score 621; DB 2;
53.6%; Pred. No. 2.5e-58;
ive 31; Mismatches 61
                                                                                                                                                                                                                                                               Human native manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                              note= "mature protein"
                                                                                                                                                                                                                                                                                                                                               "signal peptide"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                               AAW98169 standard; protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "His-163"
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Gln-143"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Asp-159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Trp-161"
                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Tyr-74"
                                                                                                                                                                                                                                                                                                                                                                                                               note= "Tyr-58"
                                                                                                                                                                                                                                                                                                                                                                               note= "His-26"
                                                                                                                                                                                                                                                                                                                                                                                              note= "His-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US018842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00927230
                                                                                                                                                                                                                                               (first entry)
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= '
.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silverman DN;
                                                                                                                                                                                                                                                                                                                                         ...24
note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYFL ) UNIV FLORIDA.
                              Local Similarity
es 118; Conserv
        Sequerice 222 AA;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09913088-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1997;
                                                                                                                                                                                                                                               05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                       Active-site
                                                                                                                                                                                                                                                                                                                                                                                        Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       Active-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nick HS,
                                                                                                                                                      181
                                                                                                                        124
                       Query Match
                                                                                                                                                                                                                               AAW981.69
                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                       Protein
                                        Matches
                                                                                                                                                                                                      AAW98169
ID AAW9
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This protein is human manganese superoxide dismutase (hWnSOD). Novel hwnSOD proteins having catalytic activity which differs from this natural hwnSOD are claimed (see AAWBSD177). The modified proteins exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hwnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. The modified hwnSOD, or expression vectors in which modified hwnSOD nucleic acid is linked to a promoter (preferably mammalian), can be used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). They can be used by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEBATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 NVTEEKYQEALAKGDVTAQIALQPALKENGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANODPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AİKRDEGSEDKEKEKLTAASVGVQGSGWGWLGENKQRGHLQIAACPNQDPLQGTTGLIPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superoxide dismutase, MnSOD, SOD, human, protein engineering, enzyme engineering, antioxidant, antiinflammatory, cytotoxicity; inflammation, reperfusion injury, therapy, mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
New recombinant human manganese superoxide dismutase proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human manganese superoxide dismutase Q143E mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 621; DB 2;
; Pred. No. 2.5e-58;
31; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25. .222
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "signal peptide"
                                                                                    Disclosure, Page 52-53; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW98175 standard; protein; 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "His-26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.9%;
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This sequence comprises both prepro- and mature-manganese super- oxide dismutase (MSOD). It is encoded by the sense strand of a double-stranded molecule contained in a recombinant vehicle. This recombinant MSOD catalyses the reaction of hydrogen ions and the SOD radical anion to form hydrogen peroxide and water. It is useful in veterinary and pharmaceutical compens. for eq reducing lesions of reperfusion following ischaemia, to prolong survival lime isolated organs and for treating inflammation. See also AAN71371-72. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
  63 NVTEEKYQEAFAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEBATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA coding for polypeptide of human manganese superoxidedismutase useful e.g. for treating inflammation, and new expression vectors and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SLSSVSROTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.7%; Score 619; DB 1; Length 222; 53.6%; Pred. No. 4.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Indels
                                                                                                          181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant human manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= mature MSOD
                                                                                                                                                                                                                                                      AAP71701 standard; protein; 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 46pp; French.
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85US-00801090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86BE-00905796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86US-00907051
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                        (revised) (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOT-) BIO-TECHNOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1987-101441/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN71370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      free radicals
                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
10-MAR-2003
14-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L2-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE905796-A.
                                                                                                                                                                                                                                                                                                       AAP71701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                               AAP7170
                                                                           à
                                                                                                                    원
                                                                                                                                                                                                                                                                                엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein is a 0143E mutant of human manganese superoxide dismutase (hhmSDD, see also AAM98170). Novel modified hhmSDD proteins having catalytic activity which differs from natural hhmSDD are claimed. The modified proteins (see also AAM9817-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hhmSDD are loadined. The chmSDD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr. 141s-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30 are located near the active site metal, are highly conserved, and are involved in a hydrogen bond relay which links the active site metal-bound hydroxyl group to ordered solvent, and are thus all potentially involved in adalytic activity, product inhibition and/or enzyme stability. Modified hhmSODs, or expression vectors in which a modified hhmSOD so expression vectors in which a modified hhmSOD or expression vectors in which a modified hhmSOD or expression vectors in which a modified hymsoD or expression or correct (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of they can be used as antioxidants in the treatment of a variety of they can be used as antioxidants in the treatment of a variety of they can be used to can be used to treat subjects suffering from, or at they can be used as antioxidants in the treatment of a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents. Note. The present sequence is not shown in the specification but is derived from the hMnSOD sequence given on page 53-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant human manganese superoxide dismutase proteins
                                                                                                                                                                     note= "Gln replaces Glu in wild-type hMnSOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.9%; Score 620; DB 2; Length 222; 53.2%; Pred. No. 3.2e-58; ive 32; Mismatches 61; Indels :
                                                                                                                       /label= Gln, Glu
                                                                                                                                                                                                                         /note= "Gln-143"
                                                                                                                                                                                                                                                                           "Asp-159"
                                                                                                                                                                                                                                                                                                                            "Trp-161"
                                                                                                                                                                                                                                                                                                                                                                             /note= "His-163"
                         /note= "Tyr-58"
                                                                        /note= "Tyr-74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US018842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00927230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.2
Matches 117; Conservative
                                                                                                                                                                                                                                                                           /note= |
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silverman DN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-229242/19.
                                                                                                                                                                                                                                                   183
                                                                                               Misc-difference
                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO9913088-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1997;
Active-site
                                              Active-site
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                                                                                                                                                                                                                                                                                                  Active-site
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decomposition of the superoxide anion to peroxide. Agents such as superoxide dismutase are able to increase the salvage of heart muscle cells. The SOD gene (AAT31018) can be used in novel therapeutic constructs also contg. a tissue-specific promoter and a hypoxia response enhancer element. Expression of the gene is enhanced in the target tissue under hypoxic conditions, such as those encountered during ischaema and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric gene contg. therapeutic gene linked to HREE - partic. for expressing SOD etc. in hypoxic tissue to reduce tissue injury caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NVNEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                             therapy; hypoxia related enhancer element; HREE; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          manganese superoxide dismutase (AAW00453) catalyses the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%; Score 618; DB 2; Length 222; 53.6%; Pred. No. 5.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                Laderoute KR,
                                                          IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA
                                                                                                                                                                                                                                                                                                                                                               reperfusion; promoter; superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 94-95; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m
                                                                                                                                                                                                                                                                                                          Human manganese superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy
                                                                                                                                                                                            Ą
                                                                                                                                                                                            AAW00453 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-IB000996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00365486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Webster KA, Bishopric NH,
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.65
Best Local Similarity 53.65
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemia or reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-321849/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT31018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRI ) SRI INT.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1994;
                                                                                                                                                                                                                                                                      26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reperfusion
                                                                                                                                                                                                                                 AAW00453;
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                       121
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                                                 Human manganese superoxide dismutase or its analogues or mutants is used generation of oxygen free radicals, eg reperfusion injury following ischaemia or organ transplant, inflammation caused by Crohn's disease or colitis, synovial inflammation induced by bacterial lipopolysaccharide endotoxin, arthritis, bronchial pulmonary displassia or lung fibrosis by radiation or an anti-neoplastic agent, eg bleomycin. It can also be used to prolong the life of excised organs. As it remains in the serum for long periods, it may be used as a long-acting therapeutic agent. Dosage is 1-200 mg/joint or 1-100, esp. 3-50, mg/kg body wt. daily. It is given intra-articularly, intratracheally, sc or iv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human manganese superoxidedismutase - used for treating e.g. injury, inflammation, arthritis, bronchial pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVTEEKYQEAFAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                           AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 223;
                                                                                                                                                                                                                                                                                                                                                                                    Human manganese superoxide dismutase; oxygen free radicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                    IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                         53.7%; Score 619; DB 1; L
53.6%; Pred. No. 4.2e-58;
live 30; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                 Human manganese superoxide dismutase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page ?; 46pp; English.
                                                                                                                                                                                                                                     AAP80551 standard, protein; 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88EP-00104880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87US-00032734.
88US-00161117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nimrod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reperfusion injury, inflamm
dysplasia or lung fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOT -) BIO-TECHNOLOGY GEN
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1988-272584/39.
N-PSDB; AAN81158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant
                                                                                                                                                                                                                                                                                                            22-0CT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1988
                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This protein is a Q143N mutant of human manganese superoxide dismutase (hMmSDD, see also AAM98170). Novel modified hMmSDD proteins having catalytic activity which differs from natural hMmSDD are claimed. The modified proteins (see also AAM98172-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMmSDD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34 and His-30 are located near the active site metal, are highly conserved, and
                                                                                                                                   Superoxide dismutase, MnSOD, SOD, human, protein engineering, enzyme engineering, antioxidant, antiinflammatory, cytotoxicity, inflammation, reperfusion injury, therapy, mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant human manganese superoxide dismutase proteins
                                                                                                                                                                                                                                                                                                                                                                                 note= "Gln replaces Asn in wild-type hMnSOD"
180 LGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMA 219
                                                                                                                  Human manganese superoxide dismutase Q143N mutant.
                                                                                                                                                                                                                                note= "signal peptide"
                                                                                                                                                                                                                                                      'note= "mature protein"
                                                                                                                                                                                                            Location/Qualifiers
1. .24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 54-55; 61pp; English.
                                                     Ā
                                                   AAW98171 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                           label= Gln, Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Trp-161"
187
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Gln-143"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Asp-159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "His-163"
                                                                                                                                                                                                                                                                                                                                        'note= "Tyr-74"
                                                                                                                                                                                                                                                                           'note= "His-26"
                                                                                                                                                                                                                                                                                               note= "His-30"
                                                                                                                                                                                                                                                                                                                   /note= "Tyr-58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US018842
                                                                                             (first entry)
                                                                                                                                                                                                                                           .222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silverman DN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-229242/19.
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1998;
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                                                                                             05-JUL-1999
                                                                                                                                                                                                                                                                Active-site
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                                                                                                                                                                                         Synthetic.
                                                                        AAW98171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nick HS,
                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                            Protein
                               RESULT 14
                                         AAW9817
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(claimed). They can also be used to treat subjects suffering from, or at risk of, cytocoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGCHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKXRAHLQIAACPNNDPLQGTTGL1PL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
are involved in a hydrogen bond relay which links the active site metalbound hydroxyl group to ordered solvent, and are thus all potentially involved in catalytic activity, product inhibition and/or enzyme stability. The particularly preferred GHJ3N mutant has a kcat of 0.3 m/sec and a kcat/km of 0.82/uM.sec compared to respective values of 40 insec and 800/uM.sec for wild-type hMmSOD. It exhibits no product inhibition. Modified hMmSODs, or expression vectors in which a modified hMmSODs nucleic acid is linked to a promoter (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superoxide dismutase, MnSOD; SOD; human; protein engineering; enzyme engineering; antioxidant; antiinflammatory; cytotoxicity; inflammation; reperfusion injury; therapy; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Gln replaces Asp in wild-type hMnSOD"
167
                                                                                                                                                                                                                                                                                                                                                                                         Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human manganese superoxide dismutase Q143D mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA
                                                                                                                                                                                                                                                                                                                                                                                     53.6%; Score 618; DB 2;
53.2%; Pred. No. 5.3e-58;
iive 31; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW98174 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "His-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tyr-58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Tyr-74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "His-26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                           Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW98174;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW9817
```

Job time : 63 secs

```
New recombinant human manganese superoxide dismutase proteins
note= "Gln-143"
        note= "Asp-159"
                           /note= "His-163"
                                                                                                             Claim 14; Page; 61pp; English.
                                                      98WO-US018842,
                                                               97US-00927230.
                  /note=
187
                                                                                  Silverman DN;
                                                                         (UYFL ) UNIV FLORIDA.
                                                                                           WPI; 1999-229242/19.
                                                                LO-SEP-1997;
                                    WO9913088-A1
                                              18-MAR-1999
             Active-site
                       Active-site
    Active-site
                                                                                  Nick HS,
```

This protein is a Q143D mutant of human manganese superoxide dismutase (hmmSDD, see also AAW98170). Novel modified hmmSDD proteins having catalytic activity which differs from natural hmmSDD are claimed. The modified proteins (see also AAW9817-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hmmSDD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-16, His-30 are located near the active site metal, are highly conserved, and are involved in a hydrogen bond relay which links the active site metal-commander involved in actalytic activity, product inhibition and/or enzyme creatalytic activity, product inhibition and/or enzyme creatalytic activity, product inhibition and/or enzyme creatalytic activity, product inhibition and/or enzyme creativity modified hwmSODs, or expression vectors in which a modified hwmSODs, or expression vectors in which a modified hwmSODs, or expression vectors in which a modified hwmSOD created to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed) and indicated the protect activity in the treatment of a variety of a such, contained the protect of the contained to the contained of a variety of the contained the contained to the contained of the contained disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents. Note. The present sequence is not shown in the specification but is derived from the hMnSOD sequence given on page 53-54

Sequence 222 AA;

```
63 NVTEBKYQBALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGB---PKGELLE 119
                                                                                                                                                                                                                                                                                                                                                    120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKXRAHLQIAACPNDDPLQGTTGLIPL 179
                                                                                                                                                                                                  64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                     124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                 S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALBPHINAQIMQLHHSKHHAAYVNNL 62
                                                                                                     6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                   10; Gaps
53.6%; Score 618; DB 2; Length 222; 53.2%; Pred. No. 5.3e-58; tive 31; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
     Query Match
Best Local Similarity 53.2
Matches 117; Conservative
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                                                                                                                                                    임
                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                          ò
```

Search completed: March 30, 2004, 17:13:08

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

March 30, 2004, 17:09:18; Search time 22 Seconds Run on:

(without alignments) 520.953 Million cell updates/sec

US-09-727-855B-5

1153 1 MSVRASLSSVSRQTFVAPAA......AAVWSVINYKEAEARLQAAL 222 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued Patents AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	, Appli		Appli	Appli	8, Appl		, Appli	8, Appl		52, Appl	⋖	5240847	, Appli	Appli	5240847	30, Appl	0, Appl	5240847	5, Appl	2227, A		17, Appl	85, App	2, Appli	6654, Ap		Ā
Description	Sequence 8	Sequence 6		Sequence 2	Sequence 2	Sequence 3	Sequence 3	Sequence 2					Sequence 2,	Sequence 7	Patent No.	Sequence 3			Sequence 7	П	C4						
ID	US-09-091-097-8	US-09-091-097-6	US-08-927-230A-2	US-09-151-052-2	US-08-365-486A-28	US-08-927-230A-3	US-09-151-052-3	US-08-880-342-28	US-08-023-980B-44	US-08-486-953A-52	US-09-126-109-2	5240847-10	US-09-075-019-2	US-09-075-019-7	5240847-11	US-08-928-692-30	US-09-339-972-30	.5240847-2	US-09-198-452A-75	US-09-489-039A-12227	US-08-445-909A-29	US-08-445-909A-17	US-08-679-493A-185	US-09-373-731-2	US-09-543-681A-6654	US-09-134-001C-3584	US-08-928-692-31
DB	4	4	~	e	(1)	~	m	m	~	N	r	9	m	m	ø	N	4	9	4	4	Н	Н	4	4	4	4	C)
% Query Match Length	224	206	222	222	222	222	222	222	222	222	222	198	198	226	198	230	230	177	214	217	204	204	196	200	224	201	233
% Query Match	60.09	58.0	54.0	54.0	53.6	53.6	ë.	53.6	53.5	53.5	53.5	52.9	52.6	52.6	52.6	49.4	49.4	46.5	44.5	43.2	43.0	42.9	41.8	41.5	41.5	40.4	40.1
Score	692	668.5	623	623	618	618	618	618	617	617	617	610	607	607	909	570	570	536	13	498.5	496	495	482.5	479	478.5	465.5	462
Result No.	н	7	æ	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 31, Appl	Sequence 24593, A	Sequence 3442, Ap	Sequence 24, Appl	Sequence 6, Appli	Sequence 4346, Ap	Sequence 4456, Ap	Sequence 9633, Ap	Sequence 24333, A	Sequence 1, Appli			Sequence 2, Appli	Sequence 52, Appl	Sequence 8, Appli	8	7	Sequence 14, Appl
US-09-339-972-31	US-09-252-991A-24593	US-09-540-236-3442	US-09-214-909-24	US-09-262-856A-6	US-09-328-352-4346	US-09-543-681A-4456	US-09-489-039A-9633	US-09-252-991A-24333	US-09-411-578-1	US-09-749-233-1	US-08-679-493A-184	US-09-008-303-2	US-09-091-097-52	US-09-458-457-8	US-09-947-199A-8	US-09-475-252-2	US-09-039-198A-14
4	4	4	4	4	4	4	4	4	ო	4	4	3	4	4	4	4	т
233	207	241	207	188	219	205	227	245	214	214	190	213	30	835	835	2016	373
40.1	40.0	39.4	38.6	37.3	31.8	31.1	30.3	29.3	28.3	28.3	27.1	17.5	9.0	9.0	0.6	8.1	7.8
462	461	454.5	444.5	430.5	367	358.5	349.5	337.5	326	326	312	201.5	104	103.5	103.5	93.5	89.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: KURODA, MASANOBU
APPLICANT: KATO, IKUNOSHIM
APPLICANT: KATO, IKUNOSHIM
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDBYO
ITILE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
ITILE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/091,097
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICALL.
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
"THEFAX: 703-205-8050
                  Sequence 8, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
                                                                        TAKESAKO, KAZUTOH
OKADO, TAKASHI
YAZHARA, TOMOKO
YAZHARA, TOMOKO
ONISHI, YOSHIMI
KATO, IKUNOSHIN
AKTYAMA, KAZUO
AKTYAMA, KAZUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 224 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-097-8
                                                                                                                                                                                                                                                                                                                                                                                             va
USA
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: V. COUNTRY:
                                                                             APPLICANT:
APPLICANT:
US-09-091-097-8
```

Score 692; DB 4; Length 224; Pred. No. 4.8e-73; 60.0%; 59.3%; Query Match Best Local Similarity 202

```
64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGHINHSIFWTNLSPNGGGE---PKGELLE 119
                                                            83 VKLOSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNAD 142
3 VMTEYTLPPLPYAYDALEPFISKEIMTVHHDKHHQTYVNNLNAAEKAYAEATAANDVLKQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 TAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SLSSVSROTFVAPPAAFQI -- RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                         US-08-927-230A-2

US-08-927-230A-2

Sequence 2, Application US/08927230A

PAUGHT NO 5985633

GENERAL INFORMATION:

APPLICANT: Nick et al.

TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESPONDENCE ADDRESS:

STREET: 28 State Street, Floor 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 623; DB 2; Length 222;
; Pred. No. 6.2e-65;
31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,230A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xaa can code for Gln or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.0%;
                                                                                                                                                                                                                       217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38, E
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 222 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.6%
Matches 118; Conservative
                                                                                                                                                                                             203 AAVWSVINYKEAEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 131
; OTHER INFORMATION:
US-08-927-230A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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      1;
                                                                                                                    67 EESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIE 126
                                                                                                                                              127 ESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIW 186
                                                                                                                                                                                                                       23 IRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQ 82
                                          11 SRQTFVAP----AAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAA 66
                                                                              6 TRRAAAAPLANAAQMGVRTKYTLPPLPYDYGALEPAISGEIMETHYEKHHRTYVNNLNAA
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
      53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KADO
APPLICANT: AKIYAMA, KADO
APPLICANT: YAMGUCHI, HIDEYO
TITILE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/091,097 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.0%; Score 668.5; DB 4; 63.1%; Pred. No. 2.5e-70; iive 24; Mismatches 47;
                                                                                                                                                                                                                                                                             187 EHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQAAL 222
                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1422-0346P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09091097
Patent No. 6432407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAKESAKO, KAZUTOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OKADO, TAKASHI
YAGIHARA, TOMOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 206 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.1:
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
COUNTRY: USA
ZIP: 22040-047
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-205-8050
          Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: TAKESA:
APPLICANT: OKADO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-091-097-6
                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-091-097-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
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63 NVNEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.6%; Score 618; DB 2; Length 222; 53.6%; Pred. No. 2.4e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
         180 LGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                 SEE: Dehlinger & Associates
: 350 Cambridge Avenue, Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Mismatches
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                                                                     RESULT 5
US-08-355-486A-28
; Sequence 28, Application US/08355486A
; Patent No. 5834306
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Patent No. 5985633
GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Mangane
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38,615
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TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 amino acids
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Matches 118; Conservative
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STREET: 350
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ZIP: 94306
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124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                       120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKXRAHLQIAACPNQDPLQGTTGLIPL 179
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53.6%; Pred. No. 6.2e-65;
Live 31; Mismatches 61; Indels 10; Gaps
                                                                                                                                                                                                                                         Sequence 2, Application US/09151052
Patent No. 6107070
GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
NUMBER OF SEQUENCES: 11
                                                                                                            181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
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UNRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,052
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OTHER INFORMATION: Xaa can code for Gln or Glu
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,230
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELEPHONE: (517)227-7400
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Floor 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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Matches 118; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Floor 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 LGIDVWEHAYYLQYKAVRPDYLKAIWNVINWENVTERYMA 219
                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,230A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa can code for Gln or Glu
US-08-927-230A-3
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street, Floor 24
                                                                                                                 ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     FILLING DATE:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: REMILIARCA, Jan.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-7400
TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
'SEQUENCE CHARACTERISTICS:
'TOWNTH' 222 amino acids
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Patent No. 6107070
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                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                             Massachusetts
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CITY: Boston
STATE: Massach
COUNTRY: USA
                                                             Boston
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US-09-151-052-3
                                                                                                   COUNTRY:
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64 NAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S AVCGISRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL 62
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53.2%; Pred. No. 2.4e-64;
tive 31; Mismatches 62; Indels 10;
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APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Keith R.
APPLICANT: Inderoute, Keith R.
APPLICANT: Green, Christopher J.
ITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                            CURPULER: ALDIA LE COMPLUER: COMPLUER: COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACEDIL Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,052
FILING DATE: US/09/151,052
FILING APPLICATION:
PRIOR APPLICATION NUMBER: 08/927,230
ATTORNEY/AGENT INFORMATION:
NAME: Remaillard, Jane
REGISTRATION NUMBER: 38,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xaa can code for Gln or Glu
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: 350 Cambridge Avenue, Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/08880342
Patent No. 6218179
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.2%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 131
OTHER INFORMATION:
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                  TELEPHONE: 617/723-4123
TELEFAX: 617/723-8962
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amino acid
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acid
                    CURRENT APPLICATION DATA
APPLICATION NUMBER: US
FILING DATE: 26-FEB-15
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                       CLASSIFICATION:
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US-08-486-953A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDFLQGTTGLIPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S AVGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL 62
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PREVENTION OF DISEASES OF CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKBIMTLHHTKHHQTYVNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: PILNO DATE: 23-JUN-1997 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER: PCT/IB95/00996 FILNO BATE: 13-NOV-1995 PRIOR APPLICATION NUMBER: US 08/365,486 FILNO BATE: 23-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 618; DB 3;
53.6%; Pred. No. 2.4e-64;
tive 31; Mismatches 61
                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION.
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08023980B
Sequence 44, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: TREATMENT AND MET
TITLE OF INVENTION: TREATMENT AND PRE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
STREET: MA
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 53.63
Matches 118; Conservative
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COMPUTER READABLE FORM:
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ZIP: 02109-1024
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63 NVTEEKYQEALAKGDVTAQTALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
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Batent No. 584920

GENERAL INFORMATION:

APPLICANT: Brown, Robert

APPLICANT: Horvitz, H. Robert

APPLICANT: Rosen, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,

TITLE OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S AVGISRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHGHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 SLSSVSRQTFVAPAAFQI -- RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.5%; Score 617; DB 2; Length 222; Best Local Similarity 53.6%; Pred. No. 3.2e-64; Matches 118; Conservative 30; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/177001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURE...
OPERATING SYSIE...
OPERATION SYSIES FASTS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
TING DATE: 07-404
UMBER: US/08/023,980B
26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTRACE: FastSed
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   44
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US Unknown

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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                      Length 222;
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APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: Shimabukuro, Michio
APPLICANT: Shimabukuro, Michio
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Gousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
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                                                                                                                                                                                                                                                                                      53.5%; Score 617; DB 2;
53.6%; Pred. No. 3.2e-64;
tive 30; Mismatches 62;
   NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/223002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
TELEPAX: 617/428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-UL-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09126109 Patent No. 6171856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                  INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acid
TYPE: amino acid
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Best Local Similarity 53.65
Matches 118; Conservative
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                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
COUNTRY: USA
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US-08-486-953A-52
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86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AVCGTSRQ.--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SLSSVSROTFVAPAAFQI - - RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
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;PATENT NO. 5240847
; APPLICANT: HECKL, KONRAD;SPEVAK, WALTER;OSTERMANN, ELINBORG
; ZOPHEL, ANDREAS;KRYSTEK, EDELTRAUD;MAURER-FOGY, INCRLD;
;WICHEL-CASTANON, MARIA J.;STRATOWA, CHRISTIAN;HAUPTWANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 LGIDVWEHAYYLQYKAVRPDYLKAIWNVINWENVTERYMA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
53.5%; Score 617; DB 3;
Best Local Similarity 53.6%; Pred. No. 3.2e-64;
Matches 118; Conservative 30; Mismatches 62;
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: MCM111ian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REPERENDE/DOCKET NUMBER: UTSD:560
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 447-777
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 AAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                             222 amino acids
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Best Local Similarity 56.1<sup>§</sup>
Matches 111, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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LENGTH: 198
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86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 VQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIFLGIDVWEHAYYLQYKNVRPDYL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAABESYSAAVGKEDVLTQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 226,
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5240847-11
;Patent No. 5240847
;Patent No. 5240847
;ADPLICANT: HECKL, KONRAD;SPEVAK, WALTER;OSTERMANN, ELINBG;ZOFFEL, MADERA;KRYSTEK, EDELTRAUD;MAURRE-FOGY, INCRID;MICHE-CASTANON, MARIA J. STRATUDAM, CHRISTIAN,HAUPTMANN, RUDOJ;MICHE-CASTANON, HANDAM MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/09/075,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%; Score 607; DB 3; 56.1%; Pred. No. 4.9e-63; tive 26; Mismatches 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%; Score 606; DB 6;
55.6%; Pred. No. 5.2e-63;
tive 28; Mismatches 54
                           E: Sheridan Ross P.C.
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFRENCE/DOCKET NUMBER: 2049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AAVWSVINYKEAEARLQA 220
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180 KAIWNVINWENVTERYMA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.1
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-075-019-7
                                                                                                                                      ZIP: 80203
COMPUTER READABLE FORM:
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Best Local Similarity
Matches 110; Conserv
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                              ADDA...
STREET: 1/v.
                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPERCOXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPERCXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHOTYVNGLNAAEESYSAAVGKEDVLTQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 607; DB 3; Length 198
56.1%; Pred. No. 4e-63;
ative 26; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/075,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848
TELECOMMUNICATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09075019
Patent No. 6190658
178 KAIWNVINWENVTERYMA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AAVWSVINYKEAEARLQA 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 111; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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CLASSIFICATION:
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                                                                                   US-09-075-019-2
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203 AAVWSVINYKEAEARLQA 220
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178 KAIWNVINWENVTERYMA 195
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Search completed: March 30, 2004, 17:13:41 Job time : 23 secs

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March 30, 2004, 17:09:18; Search time 42 Seconds (Without alignments) 1383.070 Million cell updates/sec
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1153
1 MSVRASLSSVSRQTFVAPAA......AAVWSVINYKEAEARLQAAL 222
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'(groz 6'ptodata/2'/pubpaa/PCT NEW PUB.pep:*
'(groz 6'ptodata/2'/pubpaa/USO6 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1065169 seqs, 261661801 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli Sequence 27, Appli Sequence 1, Appli Sequence 11, Appli Sequence 10, Appl Sequence 22, Appl Sequence 23, Appl Sequence 233245, Sequence 233247, Sequence 2347, Sequence 23247, Sequence 23247, Sequence 23547, Sequence 23547, Sequence 23547, Sequence 23547, Sequence 23547,	Sequence 25, Appl Sequence 24, Appl
SUMMARIES	US-09-727-8558-5 US-10-230-331-27 US-10-109-670-11 US-10-109-670-11 US-10-230-331-22 US-10-230-331-22 US-10-230-331-22 US-10-230-331-19 US-10-424-599-233245 US-10-424-599-233247 US-10-230-331-21 US-10-230-331-21	US-10-230-331-25 US-10-230-331-24
DB	01011111111111111111111111111111111111	14
% Query Match Length DB		233
% Query Match	00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	48.3
Score	1153 748 5 7 7 8 1 1 5 3 9 1 1 5 3 9 1 1 5 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	582 556.5
Result No.		14 15

Appl	Appli	Appli	Appli	ppli	ppli	pli	Ap	Appl	pli	7, A	Appl	App	App	, Ap	, Ap	3, A	App1	Appl	84,	26,	, P	ppl	62,	42,	6, 19	4 '	5, A	4, A	2, 4
75,	6, A	5, A	7, A	4, A	Sequence 3, Appli	, Ap	727,	Sequence 28, App.	Sequence 6, Appli	Sequence 12947,	23,	663,	Sequence 664, App	7867	7868	59803, A	16,	29,	Sequence 24438	2793	Sequence 59796,	Sequence 12, App	Sequence 18836	Sequence 23324	70586	5979	5979	5979	59362
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2-75	3A-6	3A-5	3A-7	3A-4	3A-3	-2	-672	1-28	9-	1-12	1 - 23	4-66	4-66	7-78	7-78	4-59	1-16	1-29	9-24	9-27	4-59	-12	9-18	9-23	4-70	4-59	4-59	4-59	4-59
9-16	0-97	0-97	0-97	0-97	0-97	-564	-626	0-33	-190	92-9	0-33	0-15	0-15	5-97	5-97	5-11	0-33	0 - 33	4-59	4-59	5-11	-333	4-59	4-59	5-11	5-11	5-11	5-11	5-11
US-10-289-762-75	US-10-130-973A-6	0-13	US-10-130-973A-7	US-10-130-973A	US-10-130-973A-3	-818	-738	0 - 23	-987	US-10-156-761-12947	0-23	0 - 31	0-31	0 - 33	0-33	0-42	0-23	0-23	0-42	0-42	0-42	-993	0-42	0-42	US-10-425-114-70586	US-10-425-114-59797	US-10-425-114-59795	US-10-425-114-59794	US-10-425-114-59362
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15	14	14	14	14	14	6	6	14	6	14	14	15	15	12	12	12	14	14	12	12	12	6	12	12	12	12	12	12	12
214	887	206	685	862	882	200	200	233	188	213	193	193	201	213	218	257	191	191	293	284	386	95	171	169	175	225	311	240	218
44.5	43.5	43.5	42.9	42.9	42.9	41.5	41.5	40.1	37.3	35.9	29.4	29.4	29.0	28.4	28.4	26.8	26.5	26.5	26.0	25.2	22.4	22.1	21.3	20.1	19.7	19.3	17.0	16.6	16.5
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513.5	502	502	495	495	49	479	479	462	430.5	414	339.5	339.5	334	327.5	327.	309.5	30	30	300	29	25	25	24	232	227.5	222	195.5	191	190.5
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MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUI
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                                  GRUERAL INC. 03.202019.03.11

APPLICANT: HOSHINO, Tatsuo
APPLICANT: HOSHINO, Tatsuo
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: PROCESS FOR THE MANUFACTU
TITLE OF INVENTION: MATERIALS THEREOF
FILE REPRENCE: C38435/111694
CURRENT PEPLICATION NUMBER: US/09/727,855B
Sequence 5, Application US/09727855B Patent No. US20020168703A1
                                                                                                                                                                                                                                                   Patentin version 3.1
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Phaffia rhodozyma
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 222; Conservative
                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                  NUMBER SOFTWARE: Pater SEQ ID NO 5
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                     85 LOSALKFNGGGHINHSLFWKNLAPYGSEFATLSEGPLKKAIBESFGSFBAFKKKFNADTA
                                                                                                     145 AVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDYLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/10109670
Publication No. US20030105283A1
Publication No. US20030105283A1
APPLICANT: TAKESAKO, KAZUTOH et al.
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
FILE REFERENCE: 1422-0523P
CURRENT APPLICATION NUMBER: US/10/109,670
CURRENT FILING DATE: 2002-04-01
                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10109670
Publication No. US20030105283A1
FUBLICATION
APPLICANT: TAKESAKO, KAZUTCH et al.
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN MALASSEZIA
FILE REFERENCE: 1422-0523P
CURRENT APPLICATION NUMBER: US/10/109,670
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EHAFYLQYKNVKADYFKAIWTVINFBEAEKRLKEAL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 692; DB 14;
59.3%; Pred. No. 4.4e-65;
iive 31; Mismatches 53;
                                                                                                                                                                                                                205 UWSVINYKEAEARLQAAL 222
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; ORGANISM: Malassezia furfur
US-10-109-670-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Malassezia furfur
US-10-109-670-11
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Best Local Similarity 63.1<sup>1</sup>
Matches 123; Conservative
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US-10-109-670-10
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Best Local (
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TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF BUKARYOTES
TILE REFERENCE: 1105.2
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR PILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 200
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Patent No. US2020168703A1

APPLICANT: HOSHINO, Tatsuo

APPLICANT: OJIMA, Kazuyuki

APPLICANT: OJIMA, Kazuyuki

APPLICANT: OJIMA, HAZUYUKI

APPLICANT: STOGUCHI, YULEA

ITILA OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFU

TITLE OF INVENTION: MATERIALS THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.42 DTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 HVLPDLPYAYNALEPFISQQIMELHHKKHHQTYVNSLNAAEQAYAKASTPKE----RIAL 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 HTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYS-AAVGKEDVLTQVKL
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71.6%; Pred. No. 3.6e-71;
"Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.3%; Score 741.5; DB 9; Length 69.7%; Pred. No. 2e-70; Live 20; Mismatches 37; Indels
FILE REFERENCE: C38435/111694
CURRENT APPLICATION NUMBER: US/09/727,855B
CURRENT FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                           ; Sequence 27, Application US/10230331; Publication No. US20030157513A1
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Ganoderma microsporum
US-10-230-331-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 LAAVWSVINYKEAEARL 218
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Best Local Similarity 69.73
Matches 138; Conservative
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Best Local Similarity 71.6
Matches 141; Conservative
                                                                                                                                                                  GENERAL INFORMATION:
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US-09-727-855B-7
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Gaps

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Sequence 19, Application US/10230331
Publication No. US20030157513A1
GENERAL INFORMATION:
APPLICANT: RAJASEMERARAN, Ram
TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF BUKARYOTES
FILE REFERENCE: 110522
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/315,757
PRIOR APPLICATION NUMBER: US 60/315,757
                                                                                                                                                                                                                                                                                    61 NGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
                                                                                                                                                                                                                                                                                                          LKKAIBESFGSFBAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH 177
                                                                                                                                                                                                                                                                                                                                                                                                66 AEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAI 125
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                                                                                                                                                                                                 1 MSVRASLSSVSRQTFVAPPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV 60
                                                                                                                                                                                                                                           1 MLSRAACST-SRRLVPALSVLGSRQKHSLPDLPYDYGALEPHINAQIMOLHHSKHHAAYV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 222;
                                                                                                                                                            63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 IPLIGIDUWEHAYYLQYKNVRPDYLKAIWNVINWENVTARYTA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%; Score 618; DB 14; 52.8%; Pred. No. 3.2e-57;
                                                                                                             54.6%; Score 629.5; DB 1454.3%; Pred. No. 1.9e-58;
                                                                                                                                                         32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Mismatches
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APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
                                                                                                                                                       Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.8 Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                          ; TYPE: PRT
; ORGANISM: BOS taurus
US-10-230-331-20
                                                                                                                                   Similarity
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US-10-424-599-233245
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US-10-230-331-19
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        LENGTH: 222
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                                                                                                                  Query Match
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Sequence 22, Application US/10230331
GENBRAL INFORMATION:
APPLICANT: RAJASEKHRAN, Ram
TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/315,757
PROR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 22
SEQ ID NO 22
LENGTH: 222
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Publication No. US20030157513A1
GENERAL INFORMATION:
ASSASSEMBRAD RAM
TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF BUKARYOTES
FILE REFERENCE: 110522
                                                                                                         63 IQLQSAIKFNGGGHINHSLFWKNLAPQSBGGGQLNDGPLKQAIEQEFGDFEKFKTTFNTK 122
                                                                                                                                                                  143 TAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
                                                                                                                                                                                            VKLOSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNAD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 YVNNLNYTBEKYHRALAKGDVTTQVALQPALKFNGGGHINHSIFWTNLSPKGGGE---PK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 GPLKKAIBESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---L 175
                          59 YVNGLNAABEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 THIPIIGVDIWEHAFFLOYKNVKPDYLAAVWSVINYKEAEAR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.0%; Score 634.5; DB 14; Best Local Similarity 55.4%; Pred. No. 5.6e-59; Matches 123; Conservative 30; Mismatches 58;
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CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/315,757
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.2
SEQ ID NO 20
                                                                                                                                                                                                                                                   203 AAVWSVINYKEAEAR 217
                                                                                                                                                                                                                                                                                ; ORGANISM: Rattus rattus
US-10-230-331-22
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APPLICATION: RALASEKHARAN, RAM
APPLICATION A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
FILE REFERENCE: 110522
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/315,757
PRIOR RILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 21
LENGTH: 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 OPALKFKGGGHINHTIFWTNLSPNGGGE---PKGELLEAIKKDFGSFDKFKERLTAVSVG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 VQCSCWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 TLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 202;
                                                                                                     Indels
                                                                            175 LTH----IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%; Score 592; DB 14;
ilarity 54.5%; Pred. No. 1.6e-54;
Conservative 29; Mismatches 55;
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US-10-310-154-662
; Sequence 662, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
   APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
   APPLICANT: Adams, Thomas H
   APPLICANT: Ruff, Thomas G.
   APPLICANT: Ruff, Thomas G.
                                                                                                                                                                                                                ; Sequence 21, Application US/10230331; Publication No. US20030157513A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 KAIWNVITWENVTERYMA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Oryctolagus cuniculus US-10-230-331-21
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Deikman, Jill
Deng, Molian
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Huang, Shihshieh
Johnson, G. Richard
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Ahrens, Jeffrey E.
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Matches 108; Conserv
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US-10-230-331-21
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APPLICANT:
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APPLICANT
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                    APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5)223) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233245
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 TANODPLITH----IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
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                                                                                                                                                                                                                                                                                                                                       52.3%; Score 603.5; DB 12; Length 240; 52.8%; Pred. No. 1.2e-55; ive 28; Mismatches 64; Indels 17;
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US-10-424-599-233247
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT MRT3847 52646C.1.pep
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                Kovalic David K
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Matches 122; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
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US-10-424-599-233247
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LENGTH: 241
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                    FEATURE:
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APPLICANT: RAJASEKHARAN, Ram
TITLE OF INVENTION: A MOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/315,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 ALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 GSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPIIGVDIWEHAFYLQYKNVKPDYLA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 BESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPII 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 TLPDLSYDFGALEPAISGEIMRLHHQKHHATYVANYNKALEQLETAVSKGDASAVVQLQA 95
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                                                                                                                                                                                                                                                                                                                                                                                 28 TLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKLQS
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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; Pred. No. 2.2e-53;
30; Mismatches 61;
                                                                                                                                                                                                                                                      50.8%; Score 586; DB 14; 57.6%; Pred. No. 8.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GIDVWEHAYYLQYKKNVKPDYLKNIWKVINWKYA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 GVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/10230331
Publication No. US20030157513A1
GENERAL INFORMATION:
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US-10-230-331-24
; Sequence 24, Application US/10230331
      NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 53.5%;
Matches 114; Conservative 3
                                                                                                                                                                                                                                                                                                                Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AVWSVINYKEA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Capsicum annuum
                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                     ORGANISM: Zea mays
                                                             SEQ ID NO 26
LENGTH: 235
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE
SEQ ID NO 25
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Sequence 26, Application US/10230331
Sequence 26, Application US/10230331
Publication No. US20030157513A1
GENERAL INFORMATION:
APPLICANT: RAJASEKHARAN, Ram
TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
FILE REFERENCE: 110522
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT FILING DATE: 2002-08-29
PRIOR RILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 KHHQTYVNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KHHATYVANYNKALEQLDAAVAKGDASAVVQLQGAIKFNGGGHVNHSIFWKNLKDISEGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ATLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVRASLSSVSRQTF-----VAPAAFQIRAKHT--LPELPYAYDALEPSISKEIMTLHHT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants FILE REPERENCE: 38-15/5296/B CURRENT APPLICATION NUMBER: US/10/310,154 CURRENT FILING DATE: 2002-12-04 PRIOR APPLICATION NUMBER: 60/337,358 PRIOR FILING DATE: 2001-12-04 NUMBER OF SEQ ID NOS: 736 SEQ ID NO 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 15; Length 233;
4.2e-54;
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52.9%; Pred. No. 4.2e
iive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                              McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parnell, Laurence D.
Start, William G.
Tennesen, Dan
                         Kretzmer, Keith A
Laccetti, Lucille B.
Lai, Chao-Qiang
                                                                                                                                                                                                                                                                                                                                          Malloy, Kathleen A.
                                                                                                                                                                                                                                               Michael M.
                                                                                                                                                                                                                                                                                                          Madson, Linda L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.9
Matches 119, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, Chunzhi
Zeng, Xiaoping
                                                                                                                                                                                     Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, Qiang
Zhao, Yajuan
Zhou, Li
Jung, Vincent
                                                                                                                                                                                                                                                                             Lund, Adrian
                                                                                                                                                 Lin, Jie-Yi
                                                                                                                           Lee, Gary
                                                                                                                                                                                                               Lu, Bin
                                                                                                                                                                                                                                         Luethy,
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US-10-310-154-662
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICAT: RAIASEKHARAN, Ram
TAPLICAT: RAIASEKHARAN, Ram
TALLE OF INVENTION:
FILE REFERENCE: 11052
CURRENT APPLICATION NUMBER: US/10/230,331
CURRENT APPLICATION NUMBER: US 60/315,757
PRIOR PELING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO. 24
LENGTH: 233
TYPE: FRT
CREATH: 233
TYPE: FRT
CREATH: 233
TYPE: FRT
CREATH: 234
TYPE: PATENTIAL ORGANISM: Pisuum sativum
US-10-230-331-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 HQTYVNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEAT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LSEG---PLKK----AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGINPLTKKLEVTTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 RASLSSVSRQ-----TFVAPAAFQIRAKH--TLPELPYAYDALEPSISKEIMTLHHTKH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
48.3%; Score 556.5; DB 14; Length 233;
Best Local Similarity 52.6%; Pred. No. 1.2e-50;
Matches 121; Conservative 28; Mismatches 48; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 ANODPLLTH----IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 --QDPLVTKGASLVPLLGIDVWEHAYXLQYKNVRPDXLKXVINWKHA 224
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Q90dj1 gallus gall
Q80zd9 melopsittac
Q9nb66 callinectes
Q7z7m4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O65324 raphanus sa
Q9m532 euphorbia e
Q8hxp5 hylobates l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8hxp2 macaca mula
Q7z7m6 homo sapien
Q7yxm5 apis mellif
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homo sapien
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1 MSVRASLSSVSRQTFVAPAA......AAVMSVINYKEAEARLQAAL
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_rvirus:*
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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739.5
644.5
643.5
637.5
625.5
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612.5
611
                                     OM protein
                                                                                                                                                                 Searched:
                                                                                                                 Sequence:
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                                                        Run on:
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7 Q8hxp7 pan troglod	98hxp6	77 07z7m7 homo sapien	094713	Q7z7m5 h	081ep0 ara	Qehxpî c		QBmuie	Q9sm64	Q873m4 m	Q9£y3	Q84v2	09618	043121	Q43803	P93606	Q43273 zea	Q9stb5	Q9f8j2 heve	Q84w70	082584	Q91yk8	09£v32	71 082571	1 087451	5 O877b6		5 Q92425	
O8HXP.	Q8HXP6	Q7Z7M7	Q947R3	Q7Z7M	QBLEPO	Q8HXP1	Q8HXP0	Q8MUI6	Q9SM64	Q873M	Q9FY.	084V	0961	0431	043803	909E6d	0432	TS60	Q9FSJ2	084W	08258	Q9LYK8	Q9FY3	082571	Q874B1	Q877B6	092464	12	
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17	18	19	20	21	22	23	24	25	56	27	78	29	30	31	32	33	34	32	36	37	38		40	41	42	43	44	45	

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ALIGNMENTS

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STRAINEBEM.F. 1767.

DOSOTETZ C.G., Goldberg D., Belinky P.A., Rothschild N., Krinfeld B., Kalati O., Burger M.,

The manganese superoxide dismutase of Phanerochaete chrysosporium:

its function, expression and gene structure.", at about a submitted (JUN-2201) to the EMBL/Geneant/DDBJ databases.

Submitted (JUN-2201) to the EMBL/Geneant/DDBJ databases.

-! FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-! CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

-! SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

-! FAMILY.
                                                                                                                                                                                        Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes,
Aphyllophorales, Corticiaceae, Phanerochaete.
NCBI_TaxID=5306;
                                          01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AP388395; AAK82369.1; -.
EMBL, AP388395; AAK82369.1; -.
GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0008382; F:inon superoxide dismutase activity; IEA.
GO; GO:0008383; F:metal ion binding; IEA.
GO; GO:0016934; F:mickel superoxide dismutase activity; IEA.
GO; GO:0016934; F:nickel superoxide dismutase activity; IEA.
GO; GO:0016931; F:oxidoreductase activity; IEA.
GO; GO:001691; F:oxidoreductase activity; IEA.
GO; GO:0016891; F:oxidoreductase activity; IEA.
Finickel Sobismutase.
Ffam; PF00081; sodfe; 1.
PFam; PF00173; sodfe; 1.
PFINTS; PR01703; MNSODISMIASE.
  206 AA
PRT;
                                      (TrEMBLrel. 19,
                                                                                                                                                                    Phanerochaete chrysosporium
PRELIMINARY;
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Q9M532

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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                        LQAALKFNGGGHINHSLFWKNLAPAASEGKGNGGVLHDGPLKKAILESFGSFENFKKEFN 119
                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYS-AAVGKEDVLTQVK 84
                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        involutus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISWUTASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacob C., Courbot M., Botton B., Chalot M., "Cloning and sequencing of a full-length cDNA encoding the manganese superoxide dismutase precursor of the ectomycorthizal fungus, Paxillus
                                                                                                                                                                                                                         141 ADTAAVQGSGWGWLGINPLTKKLEVTTTANQDPLLTHIPIIGVDIWEHAFYLQYKNVKPD
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Boletales; Paxilineae; Paxillaceae; Paxillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Manganese-superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: GO:0004785; F:copper, zinc superoxide dismutase activity; IEA. GO: GO:0008382; F:iron superoxide dismutase activity; IEA. GO: GO:0008383; F:iranganese superoxide dismutase activity; IEA. GO: GO:0046872; F:meral ion binding; IEA. GO: GO:0016594; F:mickel superoxide dismutase activity; IEA. GO: GO:0016491; F:oxidoreductase activity; IEA. GO: GO:0016491; F:oxidoreductase activity; IEA. InterPro: IPRO:0189; SODismutase. PFAm. PRO:0189; SODismutase. PFAm. PRO:0777; sodie. C. 1.
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                                                                                                              DB 3; Length 206;
                                                                                                                                                       Indels
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                                                                  63625CCFBD44A290 CRC64;
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                                                                                                                                                         27;
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Pred. No. 5.2e-59;
                                                                                                                                  Pred. No. 4.2e-60;
                                                                                                                                                       25; Mismatches
                                                                                                              Score 751.5;
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ProDom; PD000475; SODIsmutase; 1.
    PS000475; SODismutase; 1. PS00088; SOD_MN; 1.
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                                                                    206 AA; 22860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.1%;
69.3%;
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                                                                                                              65.2%;
69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF114848; AAD25353.1;
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                                                                                                                                                         Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA;
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Best Local Similarity
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                                                                                                                                  Similarity
    PD000475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=71150;
                           PROSITE, PS0000
Oxidoreductase
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                                                                       SEQUENCE
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Best Local
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                                                                                                                                                                                                                    60 LQAALRENGGGHINHSLFWKNLAPAASEGKGKGGELKPGFLKDAIDSNFGSLDSLKKEFN 119
                                                                                                                                                                                                                                                                                                                                              LOSALKFNGGCHINHSLFWKNLAPYGSE----EATLSEGPLKKAIEESFGSFEAFKKKFN 140
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                                                                                                                          59
                                                             84
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Kim H., You S., Foster L.K., Farris J., Foster D.N.;

"Expression of antioxidant genes in primary and immortal chicken embryo fibroblast cells.";

Submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MICRLASAGRSRAALVAPLGCLVARQKHTLPDLPYDYGALEPHISAEIMQLHHSKHHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VNNLNVTEEKYKEALAKGDVTAQVSLQPALKFNGGGHINHTILWTNLSPSGGGE---PKG
                                                         26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAABESYS-AAVGKEDVLTQVK
                                                                                                                                                                                                                                                                                                        141 ADTAAVQGSGWGWLGLNPLTKKLEVTTTANODPLLTHIPIIGVDIWEHAFYLQYKNVKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSVRASLSSVSRQTFVAPAAFQI-RAKHTLPBLPYAYDALEPSISKEIMTLHHTKHHQTY
                                                                                                4 QHTLPDLPYSYDALEPYVSQOIMTLHHKKHHQTYVTALNAAEVSYAKTATPKE----RIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF29388; AAK97214.1; -.
GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
GO; GO:00046872; F:manganese superoxide dismutase activity; IEA.
GO; GO:0016991; F:mickel superoxide dismutase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR001189; SODismutase.
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      32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24770 MW; A18570FC736BD3DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASOD (EC 1.15.1.1) (Superoxide dismutase [Mn/Fe]). Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 AA
      21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        201 YLAAVWSVINYKEAEARLQAAL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ProDom; PD000475; SODismutase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 YLNAIWSVINFKEAEKRFTEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 54.9%;
Matches 123; Conservative 3
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         140; Conservative
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NCBI_TaxID=9031;
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SEQUENCE FROM N.A.
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Q9NB66;
                                                                                         Q802D9
                                                                 RESULT 5
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                                                                              Q802D9
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60 VNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 PLKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                            Dismutase (MnSOD) CDNA of Chicken.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DESTROYER RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC OB BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = 0(2) + H(2)0(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                 Bu Y.Q., Luo X.G., Li S.F., Lu C., Li Y.W., Kuang X., Liu B., Li J.F.,
Yu S.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLCRLASAGRSRAALVAPWGCLVARQKHTLPDLPYDYGALEPHISAEIMQLHHSKHHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VNNLNVTEEKYKEALAKGDVTAQVSLQPALKFNGGGHINHTIFWTNLSPSGGGE---PKG
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSVRASLSSVSRQTFVAP-AAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA. GO; GO:0008382; F:copper, zinc superoxide dismutase activity; IEA. GO; GO:0008383; F:manganese superoxide dismutase activity; IEA. GO; GO:0046892; F:matcal ion binding; IEA. GO; GO:0016954; F:mickel superoxide dismutase activity; IEA. GO; GO:0016491; F:oxidoredutase activity; IEA. GO; GO:0016491; F:oxidoredutase activity; IEA. GO; GO:0006801; P:superoxide metabolism; IEA.
                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Manganese-containing superoxide dismutase precursor (EC 1.15.1.1)
                                                                                                                                                                                                                                                                                                                                                "Cloning and Sequence Analysis of Manganese-containing Superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MANGANESE-CONTAINING SUPEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.8%; Score 643.5; DB 13; July 25.8%; Pred, No. 3e-50;
                                                   177 HIPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1192114C7266687F CRC64;
                                                                                                                             224 AA
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                                                                                                                                                 (TrEMBLrel. 16, Created)
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ProDom, PD000475, SODISMUtase, 1.
PROSITE, PS00088, SOD MN, 1.
                                                                                                                                                                                                  (Superoxide dismutase [Mn/Fe]).
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Pfam; PF02777; sodfe_C; 1.
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                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                        Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                           NCBI TaxID=9031;
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                                                                                                                                      Q9DDJ1;
01-MAR-2001
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                                                                                                RESULT 4
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64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last amnotation update)
Mitochondrial manganese superoxide dismutase precursor (EC 1.15.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melopsittacus undulatus (Budgerigar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.";
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Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Callinectes
177 HIPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                 178 LIPLIGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVSQRYES 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Austad S.N., Cariberg K.,
"Melopsittacus undulatus Mn superoxide dismutase (SOD2)
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY241394; AA072712.1;
GO, GO:0004784; F:metal ion binding; IEA.
GO, GO:0006801; P:superoxide dismutase activity; IEA.
GO, GO:0006801; P:superoxide metabolism; IEA.
InterPro; IFR001189; SODismutase.
Pfam; PF00771; sodfe C; 1.
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ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD MN; 1.
SEQUENCE 224 AA; 24704 MW; F45DA30D58501D40 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mn superoxide dismutase.
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63 64

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TISSUE=Lung;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 KKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH---IPIIGVDIWEHAFYL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                         from the blue crab, Callinectes sapidus.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 SUDEROXIDE + 2 H(+) = 0(2) + H(2)0(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
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"Differential Expression of Mn-SOD Gene in Normal and Cancerous Human Mammazy Epithelial Cells.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY280721; AAP34410.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGDVSTIISLAPALKFNGGGHINHSIFWQNLSADGGE----PEGELLAAINRDFGSVENM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VAPAAFQIRAKHTLPELPYAYDALBPSISKEIMTLHHTKHHOTYVNGLNAAEESYSAAVG
                                                                                                                                                                                                                        R HSSP; P04179; 1AP6.

R GO; GC:00004785; F:croper, zinc superoxide dismutase activity; IEA.

R GO; GC:0000833; F:iron superoxide dismutase activity; IEA.

R GO; GC:000833; F:iron superoxide dismutase activity; IEA.

R GO; GC:000837; F:metal ion binding; IEA.

R GO; GC:0016491; F:oxidoreductase activity; IEA.

R GO; GC:0016491; F:oxidoreductase activity; IEA.

R GO; GC:0016891; P:oxidoreductase activity; IEA.

R Interpro; IPR01189; SODismutase.

R Pfam; PF02777; sodfe C; 1.

R PRINT; RROUTO3; MNSODISMIASE.

R PRODOM; PD0000475; SODismutase; 1.

R PROSITE; PS00088; SOD_MN; 1.
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      Brouwer M., Brouwer T.H.; "CDNA sequence of the mitochondrial manganese superoxide dismutase
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 AA; 24125 MW; A7FC7617E8908CF0 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Manganese-containing superoxide dismutase (Fragment)
SOD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.2%; Score 625.5; DB 5
56.9%; Pred. No. 1.2e-48;
iive 24; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 AA
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                                                                                                                                                                                                      AF264029; AAF74770.1; -.
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119; Conservative
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213 AA;
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SEQUENCE
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Best Local
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124 AIBESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
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                                                                                                                                                                                                                                                                                                            64 NAAEESYSAAVGKEDVLIQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
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-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = 0(2) + H(2)0(2).

-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
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R EMBL; AX267901; AAP35613.1; -.

R GO; GO:00064785; F::Copper, zinc superoxide dismutase activity; IEA.

GO; GO:0008382; F::marganese superoxide dismutase activity; IEA.

R GO; GO:0008382; F::marganese superoxide dismutase activity; IEA.

R GO; GO:00164872; F::marganese superoxide dismutase activity; IEA.

R GO; GO:0016491; F::nickel superoxide dismutase activity; IEA.

R GO; GO:0006801; P::superoxide metabolism; IEA.

R GO; GO:0006801; Sodismutase.

R Pfan; PF00081; Sodiscontase.

R Pfan; PF00081; Sodiscontase.

R Pfan; PF00081; Sodiscontase.

R Pfan; PF00081; Sodiscontase.

R Pfan; PR00777; Sodiscontase.
                                                                                                                                                                                                    6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (EC 1.15.1.1) (Superoxide dismutase [Mn/Fe])
(Superoxide dismutase 2, mitochondrial).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson
Schackwitz K.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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53.5%; Score 617; DB 4; Length 213; 53.9%; Pred. No. 7e-48;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEAR
                                                                                31; Mismatches
                                                                                Matches 117; Conservative
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                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
                                                                                                                                                                                                                                                                                                                                                                  64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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                                                                                                                                                                                                                                                                                                                                                                                                  63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
                                                                                                                                                                                                                                                                                    S AVGTSRQ--LAPVLGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
                                                                                                                                                                                                                                                       6 SLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
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                                                                                                                                                                                                  Gaps
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Macaca fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primate
                                                                                                                                                                                                  10;
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                                                                                                                                        Length 222;
                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22271545; PubMed=12383507;
Fukuhara R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of
superoxide dismutases.";
Gene 296:99-109(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00088; SOD MN; 1. SPROTIENCE 199 AA; 22340 MW; 43B9CBE138C7E563 CRC64;
                                                       Hypotherical protein, Oxidoreductase.
SEQUENCE 222 AA; 24750 MW; CA047D7900AE5905 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 296:99-109(2002).

EMBL, AB087277; BAC20366.1; -.

GO; GO:0046872; F:metal ion binding; IEA.

GO; GO:0004784; F:superoxide dismutase activity; IEA.

GO; GO:0006801; P:superoxide metabolism; IEA.

InterPro; IPR001189; SODIsmutase.

Pfam; PF02777; sodfe; 1.

PRINTS; PR01773; MNSÖDISMTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                        Score 616; DB 4;
Pred. No. 9.1e-48;
                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Mismatches
                             SOD_MN; 1.
ein; Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
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PD000475; SODismutase; 1.; PS00088; SOD_MN; 1.
                                                                                                                                        53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                                                               Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.6
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca
                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9542;
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01-OCT-2003
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                                  PROSITE;
                                                                                                                                        Query Match
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QBHXP4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 VQGSGWGWLGFNKERGQLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTBEKYQEALAKGDVTAQIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukuhara R., Tezuka T., Kageyama T.; "Structure, molecular evolution, and gene expression of primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02777; sodfe_C; 1.

PRINTS; PR01703; MNSÖDISMTASE.

PRODON; PD000475; SODIsmutase; 1.

PROSITE; PS00088; SOD MN; 1.

SEQUENCE 199 AA; 22340 MW; 43B9CBE138C7ES63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           superoxide dismutases.",

Gene 296:99-109(2002).

BMB1, AB087278; BAC2037.1; -.

GO; GO:0004784; F:suetal ion binding; IEA.

GO; GO:0004784; F:superoxide dismutase activity; IEA.

GO; GO:0006801; P:superoxide metabolism; IEA.

InterPro; IPRO1189; Sobjemutase.

Pfam; PF02777; sodfe, 1.
                                                                                                                                                                                                                                               (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                             199 AA
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                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22271545; PubMed=12383507;
                                | | : | | : | | 179 KAIWNVINWENVTERYMA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AAVWSVINYKEAEARLQA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 KAIWNVINWENVTERYMA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque)
203 AAVWSVINYKEAEARLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 112; Conservative
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                                                                                                                                                                                             PRELIMINARY;
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NCBI_TaxID=9544;
[1]
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Macaca fascicularis (Cra
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
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59 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 115
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21929762; PubMed=11932240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY329356; AAP93582.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 51.69
Matches 116; Conservative
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                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Apidae, Apis.
NCBI_TaxID=7469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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065324
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                                                                                                                                                                                                                                                                                                             2 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SLSSVSRQTFVAPAAFQI -- RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                       Fukuhara R., Tezuka T., Kageyama T.,
"Structure, molecular evolution, and gene expression of primate
"Structure, molecular evolution, and gene expression of primate
"Structure, molecular evolution, and gene expression of primate
"Structure, molecular evolution, and gene expression of primate
Gene 296:99-109 (2002).

EMBL, AB087279; BAC20358.1;
EMBL, AB087279; Finetal ion binding, IEA.

GO, GO:0004814; Fisuperoxide dismutase activity, IEA.

GO, GO:0006801; P:superoxide metabolism; IEA.

Pfam; PF00081; sodfe.

Pfam; PF00081; sodfe.

Ffam; PF02777; sodfe.

Fisuperoxide metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mukhopadhyay S., Das S.K., Mukherjee S.; "Differential Expression of Mn-SOD Gene in Normal and Cancerous Mammary Epithelial Cells"; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY280719; AAP34408.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.3%; Score 614; DB 4; Length 210; 54.7%; Pred. No. 1.3e-47; Live 31; Mismatches 55; Indels
                                                                                                                                                                                                                                            Length 199;
                                                                                                                                                                                                                                         53.3%; Score 615; DB 6; Length 19
56.6%; Pred. No. 9.6e-48;
ive 27; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22340 MW; 43B9CBE138C7E563 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Manganese-containing superoxide dismutase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA
               MEDLINE=22271545; PubMed=12383507;
                                                                                                                                                                       PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD MN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:|||::
| KAIWNVINWENVTERYMA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAVWSVINYKEAEARLOA 220
                                                                                                                                                                                                                                                       Local Similarity 56.6
Les 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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210
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                                                                                                                                                                                                                SEQUENCE
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Q7Z7M6;
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Matches
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61 NGLNAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
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                                         56 NNLNVAEEKMKEAVAKGDVNTQVALSPAIKFNGGGHLNHSIFWCNLSPNGGK----PDAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH---- 177
124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Corona M., Hughes K., Weaver D.B., Robinson G.E.; "Longevity is not associated with high antioxidant gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VSYRILFSNTVKDTFT-----RTKHTLPDLPYDYKALEPIISAEIMQLHHSKHHATYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVRASLSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whittield C.W., Band M.R., Bonaldo M.F., Kumar C.G., Liu L., Pardinas J.R., Robertson H.M., Soares M.B., Robinson G.E.; "Annotated expressed sequence tags and cDNA microarrays for studies denome Res. 12:555-566 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apis mellifera ligustica (Common honeybee).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%; Score 614; DB 5; Length 218; 51.6%; Pred. No. 1.3e-47; ive 33; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   honey bee queens.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 IPLFGIDVWEHAYYLQYKNVRPDYVKAIFDVVNWNDVNSRYKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AA; 24567 MW; 6BB7ABBB599E7C7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created) (1-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mn superoxide dismutase (Fragment).
                                                                                                                                                181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYK 212
                                                                                                                                                                                     218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AA
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Search completed: March 30, 2004, 17:10:21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 EESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 ESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPIIG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 TSFGSLEGLVKKMSAEGAAVQGSGWVWLGLDKELKKLVVDTTANQDPLVTKGGSLVPLVG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0
                                                                                                               Kwon S.-I., An C.-S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
                                                                                                                                                                                                                                                                        R HSSP, P04179; 100M.

R GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.

GO; GO:0008382; F:iron superoxide dismutase activity; IEA.

R GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.

R GO; GO:0016872; F:metal ion binding; IEA.

R GO; GO:0016891; F:nickel superoxide dismutase activity; IEA.

R GO; GO:0016891; F:superoxide metabolism; IEA.

InterPro; IPR001189; SODismutase.

R Ffam; PF00081; sodfe; 1.

R Pfam; PF00081; sodfe; 1.

R Pfam; PF000777; sodfe (C; 1.

R ProDom; PD000475; SODIsmutase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGSRSIQTP------TLPDLPYDYSALEPAISGEIMQIHHQKHHQAYVTNYNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Euphorbioideae, Euphorbieae,
              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Raphanus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD709E5DBFF81A80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%; Score 614; DB 10;
57.5%; Pred. No. 1.5e-47;
tive 20; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 IDVWEHAYYLOYKNVRPDYLKNVWKVINWKYA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
IISSUE=Underground adventitious buds;
Anderson J.V., Horvath D.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 AA; 25353 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euphorbia esula (Leafy spurge)
                                                                                                                                                                                                                                         EMBL; AF061333; AAC15806.1;
PIR; T08181; T08181.
HSSP; P04179; 1QNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                      SEQUENCE FROM N.A.
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                                                               NCBI_TaxID=3726;
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Q9M532;
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                                                                                                                                                THE
                                                                                                                                                                                                                                                                                                                                                                     RMEL, AF24310; AAF65768.1; -.
RPIR; T50830; T50830.
RPIR; T50830; T50830.
RSP; P04179; T50830.
RSP; P04179; TAP68.1; -.
RGO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
GO; GO:0008383; F:marganese superoxide dismutase activity; IEA.
GO; GO:0006801; F:mickel superoxide dismutase activity; IEA.
RGO; GO:0016491; F:nickel superoxide dismutase activity; IEA.
RGO; GO:0016491; F:superoxide metabolism; IEA.
RDITEPRO; IPR01189; SODismutase.
RP FFam; PF002777; sodfe C; 1.
RP FRINTS; PR01703; MNSODISMTASE.
RP ROSITE; PS000475; SODISmutase; 1.
RR PROSITE; PS00088; SODISmutase; 1.
RR PROSITE; PS00088; SODISmutase; 1.
RR PROSITE; PS00088; SODISmutase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LASNSAKLVSGSAVAQLRGFKTFSLPDLPYDYGALEPAISGEIMQLHHQKHHQTYITNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LSSVSRQTFVAPAAFQIRAKHT--LPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLN
                                                 Buphorbia esula (leafy spurge).";
Submitted (Mar.2000) to the BBL/GenBank/DDBJ databases.
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN TE-
CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
"Identification of mRNAs expressed in underground adventitious buds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26215 MW; 87EE25907EB702E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%; Score 612.5; DB 10; 56.3%; Pred. No. 2.1e-47; ive 25; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
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Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AA;
         SO DE RETENTANTO DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA DE LA PERSONA
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us-09-727-855b-5.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 30, 2004, 17:11:03 ; Search time 18 Seconds (without alignments) 642.199 Million cell updates/sec

US-09-727-855B-5 1153 1 MSVRASLSSVSRQTFVAPAA......AAVWSVINYKEAEARLQAAL 222 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	SODM GANMI	MOUSE P09671	P07895	P41976		ednn	_				Q8hxp7		ARATH 081235	callit	CEBAP	CAVPO P49114 cavia	Q9sm64		SODM_HEVBR P35017 hevea bras		NICPL P11796		ALIZE P41980	SODM MAIZE P09233 zea mays (m			CAPAN 049066	SODN_CAEEL P41977 caenorhabdi		SODM PENCH 075007 penicillium	000000	SODM SCHPO Q9uqx0 schizosacch
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34	556.5	48.3	245	-	SODM NEUCR	097783	neurospora
35	555.5	48.2	200	ч	SODM_AGABI	09p4t6	agaricus bi
36	535.5	46.4	205	Н	SODM CHLMU	09pka0	_
37	529.5	45.9	206	Н	SODM CHLTR	084296	chlamydia t
38	529	45.9	224	Н	SODM_CHAFE	096347	charybdis f
39	514.5	44.6	207	Н	SODM_CHLPN	Q9z9c4	chlamydia p
4 0	511	44.3	203	7	SODM_BACAA	Q811w0	
41	504.5	43.8	201	-	SODM_BACSU	P54375	bacillus su
42	503	43.6	203	Н	SODM_XANCP	P53654	xanthomonas
43	496	43.0	203	Н	SODM_BACCA	P28760	bacillus ca
44	495	42.9	203	Н	SODM_BACST	P00449	bacillus st
45	492	42.7	202	Н	SODW_LISMO	P28764	listeria mo
					ALIGNMENTS		
RESULT 1	_						

NDARD; PRT; 2 35, Created) 42, Last sequence up 42, Last sequence up 42, Last annotation rum. Basidiomycota; Hymen Basidiomycota; Hymen anodermataceae; Gano are toxic to biolo VITY: 2 superoxide + 8 1 manganese ion pe CATION: Mitochondria longs to the iron/ma commatics Institute. institutions as 1 i	Best Local Similarity 71.6%; Pred. No. 1.2e-59; Matches 141; Conservative 24; Mismatches 23; Indels 9; Gaps 3;
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                                                                                                                                                                                        201
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                                                                                            QSALKFNGGGHINHSLFWKNLAPYGSE----BATLSEGPLKKAIEESFGSFBFKKKFNA 141
                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hallewell R.A., Mullenbach G.T., Stempien M.M., Bell G.I.; "Sequence of a cDNA coding for mouse manganese superoxide dismutase."; Nucleic Acids Res. 14:9539-9539(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DECUENCE FROM N.A.

STRAIN-CSTBL/64; TISSUE-Embryo, and Kidney;

MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                          3 HVLPDLPYAYNALBPF1SQQIMELHHKKHQTYVNSLNAAEQAYAKASTPKE----RIAL
HTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYS-AAVGKEDVLTQVKL
                                                                                                                                                                                        DTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH1P11GVD1WEHAFYLQYKNVKPDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95180711; PubMed=7875582;
Jones P.L., Kucera G., Gordon H.M., Boss J.M.;
"Cloning and characterization of the murine manganous superoxide
dismutase-encoding gene.";
Gene 153:155-161(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P09671; Q64670; Q8VEM5; 01-MAR-1989 (Rel. 10, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 10-OCT-2003 (Rel. 42, Last amnotation update) Superoxide dismutase (Mn], mitochondrial precursor (EC 1.15.1.1) SOD2 OR SOD-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sun Y., Hegamyer G., Colburn N.M.; "Sequence of manganese superoxide dismutase-encoding cDNAs from multiple mouse organs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disilvestre D., Kleeberger S.R., Johns J., Levitt R.C., "Structure and DNA sequence of the mouse MnSOD gene."; Mamm. Genome 6:281-284(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                222 AA
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STRAIN=BALB/c, and C3H;
MEDLINE=94010326; PubMed=8406027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=87091590; PubMed=3797253;
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                                                                                                                                                                                                                                                                                  202 LAAVWSVINYKEAEARL 218
                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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RAM Rectione P., Risis B. Ringshald M., Rodriguez I., Schwarch E.,

Rasaki H., Sato M., Schoenbech C., Soya T., Shibata Y., Storch K.P.,

Rasaki H., Toyoco A.K., Wang R.H., Warticles I. W. Willams I.,

Ray Marchichmi L., Sato M., Schoenbech C., Soya T., Shibata Y., Storch K.P.,

Ray Marchichmi L., Sato M., Schoenbech C., Soya T., Shibata Y., Storch K.P.,

Ray Marchichmi L., Sato M., Tokichmi R.H., Warticles C., Willams I.,

Ray Martine A.O., Soing T., Shibata Y., Storch K.P.,

Ray Martine A.O., Soing T., Shibata Y., Storch K.P.,

Ray Martine A.O., Soing T., Shibata Y., Storch K.P.,

Ray Martine A.O., Soing T., Shibata Y., Storch K.P.,

Ray Martine A.O., Soing T., Shibata Y., Storch K.P.,

Ray Martine A.O., Marusina R., Paring B., Bartow K.H., Schoefer C.F., Bhar N. Y.,

Ray Martine A.O., Marusina K., Paring B., Bartow K.H., Schwefer C.F., Bhar N. Y.,

Ray Martine A.O., Marusina K., Paring B., Bartow K.H., Schwefer C.F., Bartow K.H.,

Ray Marchenol M., Sookers M.B., Boraddo M.P., Rodrigues S., Sanchez A.,

Ray Ray B., Ray M., Martine A., Young D., Schwefer C. M., Martine M.,

Ray R. S., Loquellano N.K., Storch E.D., Martine M. O., Martine M. A.,

Ray R. S., Rodrigues A.C., Storwed M.B., Sookers M.B., Boraddo M.Y., Martine M.,

Ray M. M., Martine M. W., Tokichman J.M., Young A.C., Shewhenko Y., Bolfata G.G.,

Ray R. S., Rodrigues A.C., Storwed M.B., Shaka B., Martine M., Martine M., M., Carly L.J., Martine M.,

Ray M. M., Martine M. W., Martine M., W., Carly L.J., Martine M.,

Ray R. S., Rodrigues A.C., Storwed M.B., Shaka B., M., Carly L.J., Martine M.,

Ray M. M., M., Martine M., W., Shaka B., M., Shaka B., M., Shaka B., ```

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PRT;
 MEDLINE=94121934; PubMed=8292376;
 24674 MW;
 55.0%;
 EMBL; Y00497; CAA68549.1; -. EMBL; X56600; CAA39937.1; -.
 Matches 123; Conservative
 STANDARD;
 24
222
50
98
183
167
 167 1
222 AA;
 Bos taurus (Bovine).
 Similarity
 SEQUENCE FROM N.A.
TISSUE=Lung;
 Transit peptide
TRANSIT
 SODM BOVIN
P41976;
01-NOV-1995 (
01-NOV-1995 (
10-OCT-2003 (
 METAL
CONFLICT
 Query Match
Best Local S
 SEQUENCE
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 61 NGLNAAEESYSAAVGKEDVLIQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
 60 NNINATEEKYHEALAKGDVTTQVALQPALKFNGGGHINHTIFWTNLSPKGGGE---PKGE 116
 121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH 177
 1 MSVRASLSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV 60
 superoxide dismutase.";
Am. J. Respir. Cell Mol. Biol. 4.278-286(1991).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COPACTOR: Binds 1 manganese ion per subunit (By similarity).
 STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=91159005; PubMed=2001291;
HO Y.-S., Howard A.J., Crapo J.D.;
"Molecular structure of a functional rat gene for manganese-containing
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
 STRAIN=Sprague-Dawley, TISSUE-Liver,
MEDLINE=88096516; PubMed=3697077;
HO Y.-S., Crapo J.D.,
"Nucleotide sequences of cDNAs coding for rat manganese-containing
 01-MAY-1998 (Rel. 08, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (BC 1.15.1.1)
 7 ;
 222;
 222 SUPEROXIDE DISMUTASE [WN].
50 MANGANESE (BY SIMILARITY).
98 MANGANESE (BY SIMILARITY).
183 MANGANESE (BY SIMILARITY).
187 MANGANESE (BY SIMILARITY).
187 MANGANESE (BY SIMILARITY).
5 A -> G (IN REF. 5; AAH18173).
18 G -> V (IN REF. 1).
138 V -> M (IN REF. 1).
24603 MW; 9AE804CS5A8357D9 CRC64;
 DB 1; Length
Pfam; PF02777; sodfe_C; 1.
PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODISMTASE; 1.
PROSITE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 Indels
 178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 55.0%; Score 634.5; DB 1;
55.6%; Pred. No. 2e-49;
... Mismatches 62;
 SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Mitochondrial matrix.
 222 AA
 MITOCHONDRION
 Nucleic Acids Res. 15:10070-10070(1987)
 PRT;
 Best Local Similarity 55.5 Matches 124; Conservative
 STANDARD;
 Rattus norvegicus (Rat).
 superoxide dismutase.";
 24
222
50
50
98
183
 138 1
222 AA;
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 Transit peptide
TRANSIT
 18
 SODM RAT
P07895;
 CONFLICT
 SEQUENCE
 Query Match
 METAL
METAL
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 CHAIN
 SODM_RAT
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 59 YVNGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSE 118
 119 GPLKKAIEESFGSFEAFKKKENADTAAVQGSGWGWIGLNPLTKKLEVTTTANQDPL---L 175
 115 GELLEAIKRDFGSFEKFKEKLTAVSVGVQGSGWGWLGFNKEQGRLQIAACSNQDPLQGTT 174
 00
00
 57
 58 YWNLAVTEEKYHEALAKGDVTTQVALQPALKFNGGGHINHSIFWTNLSPKGGGE---PK
 1 MLCRAACSAGRE---LGPAASTAGSRHKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAT
 1 MSVRASLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQT
 Gaps
SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
MCBI_TaxID=9913,
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 11;
 Meyrick B., Magnuson M.A., \fi "Identification and functional characterization of the bovine
 Score 634.5; DB 1; Length 222; Pred. No. 2e-49;
 Indels
 PIR; S21661; DSRTN.
HSSP; P04179; 1ABM.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe_C; 1.
Pfam; PF00777; sodfe_C; 1.
PRINTS; PR01703; MNSODISMTASE.
PRODOM; PD000475; SODISmutase; 1.
PROSITE; PS00088; SOD MN; 1.
 SUPEROXIDE DISMUTASE [MN].
MANGARESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
Q -> H (IN REF. 1).
 176 THIPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEAR 217
 GLIPLIGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVSQR 216
 58;
 222 AA
 30; Mismatches
 MITOCHONDRION
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sapiens (Human)
 NCBI_TaxID=9606;
 TISSUE=Colon;
 Church S.L.;
 8
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M
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
 60 NNLNVAEEKYREALEKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PQGE 116
 61 NGLINAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
 121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH 177
 9
 59
manganous superoxide dismutase promoter.";
Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CAPALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COPACTOR: Binds 1 manganese ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.
 1 MSVRASLSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV
 Gaps
 STANDARD; PRT; 222 AA.

SOOM HUMAN STANDARD; Q99223;
20-MAR-1987 (Rel. 04, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
SOD2.
 DB 1; Length 222;
 MITOCHONDRION (BY SIMILARITY).
SUPERCAIDE DISWUTASE [MN].
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
S -> R (IN REF. 1; AAD14001).
F -> V (IN REF. 1; AAD14001).
W., 806CC3FCB1A74413 CRC64;
 Indels
 PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODISMTEASE; 1.
PROSITE, PS00088; SOD. MN: 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 63;
 54.6%; Score 629.5; DB 1
54.3%; Pred. No. 5.5e-49;
 32; Mismatches
 EMBL; L22092; AAA30655.1; ALT_INIT.
EMBL; L22093; AAA30656.1; --
EMBL; S67818; AAC60522.2; --
EMBL; S67819; AAD14001.1; --
PIR; 151918; IS1918.
HSSP; P04179; 1ABM.
 InterPro; IPR001189; SODismutase.
Pfam; PP00081; Sodfe; 1.
Pfam; PF02777; Sodfe_C; 1.
 90 F
24638 MW;
 Query Match
Best Local Similarity 54.3[†]
Matches 121; Conservative
 24
222
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98
183
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222 AA;
 Transit peptide.
 25
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Ho Y.-S., Crapo J. D.; Laboline complementary DNAs encoding human manganese-containing superoxide dismutase."; FEBS Lett. 229:256-260(1988).
 SEQUENCE OF 25-222.
MEDLINE=85030346; PubMed=6386798;
Barra D., Schinina M.E., Simmaco M., Bannister J.V., Bannister W.H., Rotilio G., Bossa F.;
"The primary structure of human liver manganese superoxide dismutase.";
 "Isolation of cDNAs encoding human manganese superoxide dismutase.";
Nucleic Acids Res. 16:6224-6224(1988).
 MEDLINE=91105727; PubMed=1988135; St Clair D.K., Holland J.C.; "Complementary DNA encoding human colon cancer manganese superoxide dismutase and the expression of its gene in human cells."; Cancer Res. 51:939-943(1991).
 TISSUB=Heart;
MEDLINE=25203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
 "Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of a cDNA encoding a new human transcript."; Biochim. Biophys. Acta 1087:250-252(1990).
 SEQUENCE FROM N.A.
MEDDINE-889076921; PubMed-2462451;
Wispe J.R., Clark J.C., Burhans M.S., Kropp K.E., Korfhagen T.R.,
Whiteett J.A.;
Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
 M., Hartman J.R.;
 Wan X.S., Devalaraja M.N., St Clair D.K.; "Molecular structure and organization of the human manganese superoxide dismutase gene.";
 "Synthesis and processing of the precursor for human mangano-superoxide dismutase.";
 Beck Y., Oren R., Amit B., Levanon A., Gorecki M
"Human Mn superoxide dismutase cDNA sequence.";
Nucleic Acids Res. 15:9076-9076(1987).
 Biochim. Biophys. Acta 994:30-36(1989).
 SEQUENCE FROM N.A., AND VARIANT VAL-16.
MEDLINE=88289364; PubMed=3399391;
 Biol. Chem. 259:12595-12601(1984).
 Electrophoresis 15:1459-1465(1994)
 Cell Biol, 13:1127-1136(1994).
 MEDLINE=95217333; PubMed=7702755;
 SEQUENCE FROM N.A. MEDLINE=91027939; PubMed=1699607;
 MEDLINE=88067716; PubMed=3684581;
 SEQUENCE FROM N.A.
TISSUE-Liver;
MEDLINE-88152250; PubMed=2831093;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 [9]
SEQUENCE OF 25-39.
 SEQUENCE FROM N.A.
 [10]
SEQUENCE OF 25-39.
TISSUE=Heart;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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PRT;
 EMBL; X07834; CAA30687.1; -.
EMBL; M36693; AAA36622.1; -.
EMBL; X15132; CAA33228.1; -.
EMBL; X14322; CAA32502.1; -.
EMBL; S77127; AAD14248.1; ALT_SEQ.
 InterPro; IPR001189; SODismutase.
 Transit peptide; 3D-structure;
TRANSIT 1 24 MI
 EMBL; X59445; CAA42066.1; -.
 EMBL; Y00472; CAA68533.1; -. EMBL; Y00985; CAA68791.1; -.
 SWISS-2DPAGE; P04179; HUMAN.
 HSC-2DPAGE; P04179; HUMAN.
 118; Conservative
 STANDARD;
 PMMA-2DPAGE; P04179; -. Siena-2DPAGE; P04179; -
 Genew; HGNC:11180; SOD2
 Pfam; PF00081; sodfe; 1
Pfam; PF02777; sodfe_C;
 1MSD; 15-JUL-93.
1N0J; 06-NOV-02.
 1AP5; 28-JAN-98,
1AP6; 28-JAN-98
 15M1; 01-SEP-00.
 1VAR; 10-JUN-96
 1LUV; 19-JUN-02
 1LUW; 19-JUN-02
 06-NOV-02
 S17127; AAD14
S13162; DSHUN.
 Best Local Similarity
 147460;
 10NM;
 SODM HORSE
Q9XS41;
 1NON;
 Query Match
 SODM_HORSE
 PIR;
PDB;
PDB;
PDB;
PDB;
 PDB;
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 Matches
 RESULT 6
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 -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYNIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- CORCTOR: Binds I manganese ion per subunit.
-!- SUBUNIT: Homoretramer.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SUBCELLULAR Belongs to the iron/manganese superoxide dismutase
 MEDLINE=20311275; PubMed=10852710; Leveque V.J.-P., Stroupe M.E., Lepock J.R., Cabelli D.E., Tainer J.A., Nick H.S., Silverman D.N.; "Multiple replacements of glutamine 143 in human manganese superoxide dismutase: Effects on structure, stability, and catalysis."; Biochemistry 39:7131-7137(2000).
 Hsieh Y., Guan Y., Tu C., Bratt P.J., Angerhofer A., Lepock J.R., Hiddey M.J., Tainer J.A., Nick H.S., Silverman D.N.; "Probing the active site of human manganese superoxide dismutase: the role of glutamine 143.";
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=93008233; PubMed=1394426;
MEDLINE=93008233; PubMed=1394426;
Bargstahl G.E.O., Parge H.E., Hickey M.J., Beyer W.F. Jr.,
Hallewell R.A., Tainer J.A.;
"The structure of human mitochondrial manganese superoxide dismutase
reveals a novel tetrameric interface of two 4-helix bundles.";
Cell 71:107-118(1992).
 'Kinetic analysis of product inhibition in human manganese superoxide
 MEDLINE=98206887; PubMed=9537987; Guan Y., Hickey M.J., Borgetahl G.E.O., Hallewell R.A., Lepock J.R., O'Connor D., Hsieh Y., Nick H.S., Silverman D.N., Tainer J.A.; Crystal structure of Y34F mutant human mitochondrial manganese superoxide dismutase and the functional role of tyrosine 34."; Biochemistry 37:4722-4730(1998).
 TISSUE=Breast carcinoma;
MEDLINE=97295304; PubMed=9150946;
Rasmuseen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
Simpson R.J., Dorow D.S.;
"Two-dimensional electrophoretic analysis of human breast carcinoma proteins; mapping of proteins that bind to the SH3 domain of mixed
 Kovalyov L.I., Shishkin 8.S., Efimochkin A.S., Kovalyova M.A., Esbova E.S., Egorov T.A., Musalyamov A.K.; "The major protein expression profile and two-dimensional protein database of human heart.";
 variant Ile58Thr reduces activity by destabilizing the tetrameric
 X-RAY CRYSTALLOGRAPHY (2.12 ANGSTROMS) OF MUTANT ALA-185.
MEDLINE=21464436; PubMed=11580280;
Hearn A.S., Stroupe M.E., Cabelli D.E., Lepock J.R., Tainer J.A., Nick H.S., Silverman D.N.;
 "Human mitochondrial manganese superoxide dismutase polymorphic
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF VARIANT ASN-167
 X-RAY CRYSTALLOGRAPHY (2.13 ANGSTROMS) OF MUTANT ALA-167.
 MEDLINE=96183289; PubMed=8605177;
Borgstahl G.E.O., Parge H.E., Hickey M.J., Johnson M.J.,
Boissinot M., Hallewell R.A., Lepock J.R., Cabelli D.E.,
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF VARIANT THR-82.
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANT TYR-58
 Electrophoresis 16:1160-1169(1995)
 Biochemistry 40:12051-12058(2001).
 MEDLINE=98206888; PubMed=9537988;
MEDLINE=96007936; Pubmed=7498159
 Electrophoresis 18:588-598(1997)
 Biochemistry 35:4287-4297(1996).
 Biochemistry 37:4731-4739(1998).
 ineage kinase MLK2
 SEQUENCE OF 25-39.
 Tainer J.A.;
 dismutase.";
 interface."
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 64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
 124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPI 180
 120 AIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPL 179
 63
 62
 63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE
 S AVCGTSRQ--LAPALGYLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNL
 6 SLSSVSROTFVAPAAFQI - - RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
 Gaps
 10;
 MIM; 147460; -.
GO; GO:0006979; F:manganese superoxide dismutase activity; NAS.
GO; GO:0006979; P:response to oxidative stress; NAS.
 53.8%; Score 620; DB 1; Length 222;
53.6%; Pred. No. 3.9e-48;
Live 31; Mismatches 61; Indels
 PRINTS, PR01703; MNSODISMTASE.
Probom; PD000475; SODISMTASE, 1.
PROSITE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 180 LGIDVWEHAYYLQYXXVVRPDYLKAIWNVINWENVTERYMA 219
 181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 ¥
 Polymorphism. MITOCHONDRION.
 222
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SODM MACFA
 98
 178
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 3,
 NGINAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
 60 NNLNVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHTIFWTNLSPNGGGE---PKGK 116
 121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH 177
 9
 59
 MEDLINE=99261591; PubMed=10331206;
Ishida N., Katayama Y., Sato F., Hasegawa T., Mukoyama H.;
"The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD and
Mn-SOD, and these expressions in equine tissues.";
J. Vet. Med. Sci. 61:291-294(1999)
 -: FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-: CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-: COFACTOR: Binds 1 manganese ion per subunit (By similarity).
-: SUBUNIT: Honoterramer (By similarity).
-: SUBCELLULAR LOCATION: Mitcohondrial matrix.
-: SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 1 MSVRASLSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
 Last sequence update)
Last annotation update)
[Mn], mitochondrial precursor (EC 1.15.1.1)
 1,
 DB 1; Length 222;
 MITOCHONDRION (BY SIMILARITY)
 Indels
 177 IPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVSERYMA 219
 Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 SUPERCOXIDE DISMUTASE [MN]
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
 178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 93A069481944E98C CRC64;
 99
 53.4%; Score 615.5; DB 1
52.9%; Pred. No. 9.8e-48;
 32; Mismatches
 InterPro; IRR001189; SODismutase. Pfam; PP00081; sodfe; 1. Pfam; PP02777; sodfe C; 1. PRIMTS; PR01703; MNSODISMTASE. ProDom; PD0000475; SODismutase; 1. PROSITE; PS00088; SOD_MN; 1.
 EMBL; AB001693; BAA76922.1; -.
 Created)
 24739 MW;
 Matches 118; Conservative
 24
222
50
50
98
183
 Equus caballus (Horse)
16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 10-OCT-2003 (Rel. 42,
 Supercxide dismutase
 222 AA;
 Similarity
 HSSP; P04179; 1ABM
 SEQUENCE FROM N.A.
 NCBI_TaxID=9796;
 Transit peptide.
TRANSIT
 25
50
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183
 TISSUE=Testis;
 family.
 (Mn-SOD).
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 2
 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 61 OPALKFNGGGHINHSIFWINLSPNGGGE---PKGELLEAIKRDFGSFEKFKEKLTAASVG 117
 146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 85
 09
 -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
-!- SUBUNIT: Homoterramer (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 1 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 Gaps
 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
 SEQUENCE FROM N.A.
MEDLINE-22271545; PubMed=12383507;
FURUMARA R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate superoxide dismutases.";
 . 9
 53.3%; Score 615; DB 1; Length 198; 56.6%; Pred. No. 9.4e-48; ive 27; Mismatches 53; Indels
 EMBL, AB087278, BAC20357.1, ALT INIT.
InterPro, IPR001189; SODismutase.
Pfam, PF00018, Sodfe; 1.
Pfam, PF00777; sodfe; 1.
PRINTS, PR01703, MNSODISMTASE.
ProDom, PD000475; SODISMITASE.
PROSTIE; PS00089; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase (Mn], mitochondrial (EC 1.15.1.1).
 FB4F6B063198E5CC CRC64;
198 AA
 203 AAVWSVINYKEAEARLQA 220
 KAIWNVINWENVTERYMA 195
 22209 MW;
 Matches 112; Conservative
 STANDARD;
 Cercopithecinae; Macaca.
 Gene 296:99-109(2002).
 163
 159 1
163 1
198 AA;
 Local Similarity
 NCBI TaxID=9541;
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15-MAR-2004
 SODM_MACMU
 112;
 98
 SEQUENCE
 Query Match
 OBHXP2;
 SODM MACMU
 METAL
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 Matches
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 3
 61 QPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLEAIKRDFGSFEKFKEKLTAASVG 117
 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 9
 -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 1 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
 Gaps
 Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 SEQUENCE FROM N.A.
MEDLINE=22271545; PubMed=12383507;
Fukuhara R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
 9
 EMBL; AB087277; BAC20356.1; ALT INIT.

InterPro; IPR001189; SODismutase.

Ffam; PF00777; sodie C; 1.

Fram; PF00777; sodie C; 1.

FRINTS; PR01703; MNSÖDISMTASE.

PRODOM; PD000475; SODISmutase; 1.

FROSITE; PS00088; SOD MN; 1.

Oxidoreductase; Metal-binding; Manganese; Mitochondrion.

METAL 26 26 MANGANESE (BY SIMILARITY).

METAL 159 159 MANGANESE (BY SIMILARITY).

METAL 163 163 MANGANESE (BY SIMILARITY).

METAL 163 MANGANESE (BY SIMILARITY).

METAL 163 MANGANESE (BY SIMILARITY).

METAL 163 MANGANESE (BY SIMILARITY).
 Length 198;
 53; Indels
 Q8HXP4;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)
 FB4F6B063198E5CC CRC64;
 53.3%; Score 615; DB 1; 56.6%; Pred. No. 9.4e-48;
 198 AA
 27; Mismatches
 or send an email to license@isb-sib.ch).
 203 AAVWSVINYKEAEARLQA 220
 178 KAIWNVINWENVTERYMA 195
 22209 MW;
 Conservative
 superoxide dismutases.";
Gene 296:99-109(2002).
 Cercopithecinae; Macaca.
 159 1
163 1
198 AA;
 Local Similarity
 NCBI TaxID=9543
 Matches 112;
 SODM MACFU
 98
 SEQUENCE
 Query Match
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 61 QPALKFNGGGHINHSIFWTNLSPNGGGE---PKGBLLEAIKRDFGSFEKFKEKLTAASVG 117
 OSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 146 VQGSGWGWLGLNPLTXKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 9
 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 Gaps
 Gene 296:99-109(2002).
-!-FUNCTION: Destroys radicals which are normally produced within tells and which are toxic to biological systems
-!-CATALTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!-COFACTOR: Binds 1 manganese ion per subunit (By similarity).
-!-SUBUNIT: Homocetzamer (By similarity).
-!-SUBCELDULAR LOCATION: Mitcohodrial matrix (By similarity).
-!-SUBCELDULAR LOCATION: Mitcohodrial matrix (By similarity).
 Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 MEDLINE=22271545; PubMed=12383507;
Pukuhara R., Peruka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
superoxide dismutases.";
 . 9
 Length 198;
 EMBL, AB087279; BAC20358.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PR00081; SODfe; 1.
PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODismutase; 1.
PR0STTE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 53; Indels
 MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
 (BY SIMILARITY).
 15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)
 163 163 MANGANESE (BY SIMILARITY)
198 AA; 22209 MW; FB4F6B063198E5CC CRC64;
 53.3%; Score 615; DB 1; 56.6%; Pred. No. 9.4e-48;
198 AA
 Last sequence update)
 27; Mismatches
 MANGANESE
MANGANESE
 203 AAVWSVINYKEAEARLQA 220
 178 KAIWNVINWENVTERYMA 195
 15-MAR-2004 (Rel. 43, Created)
 Conservative
STANDARD;
 Cercopithecinae; Macaca.
 (Rel. 43, (Rel. 43,
 SEQUENCE FROM N.A.
 Best Local Similarity
 NCBI_TaxID=9544;
 159
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26
 98
 178
 SEQUENCE
 Query Match
 Matches
 SODM_PANTR
RESULT 11
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 7
 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 9
 Superior distributions: (Gene 296:99-109(2002).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COPACTOR: Binds 1 manganese ion per subunit (By similarity).
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- SUBCELLULAR: Delongs to the iron/manganese superoxide dismutase
 26 KHTLPELPYAYDALBPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 1 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
 Gaps
 Hylobates lar (Common gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
 MEDLINE-22271545; PubMed-12383507;
Fukuhara R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
 . 9
 Length 198;
 54; Indels
 Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
 15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (BC 1.15.1.1).
 22234 MW; E266AFBBBDB34566 CRC64;
 53.0%; Score 611; DB 1; 56.1%; Pred. No. 2.1e-47;
 198 AA
 27; Mismatches
 EMBL, AB087276; BAC20355.1; ALT INIT.
InterPro; IPR001189; SODismutasē.
Pfam; PP00081; sodfe; 1.
Pfam; PF02777; sodfe; 1.
PRINTS; PR01703; MNSÖDISMTASE.
ProDcm; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD_MN; 1.
 203 AAVWSVINYKEAEARLQA 220
 178 KAIWNVINWENVTERYMA 195
 (Rel. 43, Created)
 Conservative
 superoxide dismutases.";
 STANDARD;
 159
163
 163 1
198 AA;
 Query Match
Best Local Similarity
Matches 111; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=9580;
 159
 15-MAR-2004
 SODM HYLLA
Q8HXP5;
 86
 61
 SEQUENCE
 146
 SODM HYLLA
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 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 61 QPALKFNGGGHINHSIFWINLSPNGGGE---PKGELLEAIKRDFGSFDKFKEKLTAASVG 117
 09
 85
 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 Gaps
 Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
 MEDLINE=22271545; PubMed=12383507;
Fukuhara R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
 . 9
 EMBL; AB087274; BAC20353.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; Sodfe; 1.
Pfam; PF00277; Sodfe C; 1.
PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODJSmutase; 1.
PROSITE; P800089; SOD_MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
METAL
 54; Indels
 MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
 15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)
 198 AA; 22204 MW; F772EABBA6A9F4CD CRC64;
 52.9%; Score 610; DB 1; 56.1%; Pred. No. 2.6e-47;
 198 AA
 Mismatches
 27;
 |:|:||| | KAIWNVINWENVTERYMA 195
 203 AAVWSVINYKEAEARLQA 220
 15-MAR-2004 (Rel. 43, Created)
 Conservative
 STANDARD;
 159
163
 Similarity
 SEQUENCE FROM N.A.
 159
 NCBI_TaxID=9598;
SODM PANTR
Q8HXP7;
 Local Sim
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RESULT 12

231 AA

PRT;

STANDARD;

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thaliana
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 2
 86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 61 ÓPÁLKFNGGGHÍNHSIFWINLSPNGGGE---PKGELLEAIKRDFGSFDKFKEKLTÁASVG 117
 146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 85
 9
 Gene 296:99-109(2002).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- CAPACTOR: Bainds I manganese ion per subunit (By similarity).
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 1 KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIAL
 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 Gaps
 -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
 . 9
 MEDLINE=22271545; PubMed=12383507;
Fukuhara R., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
 EMBL; Abv.

InterPro; IPR001189, ____
R Pfam; PR002777; sodfe C; 1.

DR PRINTS; PR01703; MNSODISMTASE.

DR Probom; PR000475; SODismutase; 1.

DR PROSTIE; PS00048; SODismutase; 1.

DR PROSTIE; PS00088; SOD MN;

RW Oxidoreductase; Metal-Dinding; Manganese; Mitochondrion.

TA 74 MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).
 Length 198;
 54; Indels
 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 , Pred. No. 2.6e-47; 27; Mismatches 54
 52.9%; Score 610; DB 1; 56.1%; Pred. No. 2.6e-47;
 198 AA
 203 AAVWSVINYKEAEARLOA 220
 178 KAIWNVINWENVTERYMA 195
 Query Match 52.9%;
Best Local Similarity 56.1%;
Matches 111; Conservative
 superoxide dismutases.";
 STANDARD;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9600;
 family
 SODM_PONPY
 SODM
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SODM\_ARATH RESULT 13

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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Ralanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
Ralanoubat M., Lemcke K., Rieger M., Parez-Alonso M., Obermaier B.,
Bolseny M., Boutry M., Grivell L.A., Mache R., Pusdomench P.,
Ra Belseny M., Boutry M., Artiguenave F., Robert C., Brottier F.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,
Ra Wincheller-Auer S., Gabel C., Pench M., Bense V.,
Wurmbach B., Draonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Wickelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Weichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,
Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,
R. Mavarro P., Collado C., Perez-Perez A., Ottelmwelder B., Duchemin D.,
R. Mannhaupt G., Haase D., Schoof H., Rod H., Tallon L.J., Jenkins J.,
R. Rooney T., Rizzo M., Walte A., Wu D., Koo H.L., Tallon L.J., Jenkins J.,
R. Rooney T., Rizzo M., Waltis A., Uhterback T., Fujii C.Y., Shea T.P.,
R. Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
R. Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.,
R. Sasamoto S., Kimura T., Idesawa K., Kabori B., Marania B.,
R. Kiyokawa C., Kohara M., Marcumoro M., Matchin G., Watanabe A., Yamada M., Tanda M., Tabata S.,
R. Astanabe A., Yamada M., Tanda M., Tabata S.,
R. Tageluence and analysis of chromosome 3 of the plant Arabidopsis
 STRAINECY. Columbia;

X MEDLINE=22954850; PubMed=14593172;

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Rarlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Torluni M.J.,

A chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A chan M.M., Tang C.C., Onodera L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A xamiya A., Meyers C., Nakajima M., Narusaka M., Saki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender B.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
 -i- FUNCTION: Destroys radicals which are normally produced within the
 Kliebenstein D.J., Monde R.A., Last R.L., "Superoxide dismutase in Arabidopsis: an eclectic enzyme family with disparate regulation and protein localization."; Plant Physiol. 118:637-650(1998).
0912<u>15</u>; Q9SRR3; Created)
16-OCT-2011 (Rel. 40, Created)
18-MAR-2004 (Rel. 41, Last sequence update)
11-MAR-2004 (Rel. 43, Last annocation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
SODA OR MSDI OR AT3G10920 OR F9PR.26.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eucosids II; Brassicales; Brassicaceae, Arabidopsis.
 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
 STRAIN=cv. Columbia;
MEDLINE=98440686; PubMed=9765550;
 Nature 408:820-822(2000).
 Science 302:842-846(2003)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 genome.";
```

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PRT;
 203 AAVWSVINYKEAEARLQA 220
 178 KAIWNVINWENVTERYMA 195
 198 AA;, 22248 MW;
 Matches 110; Conservative
 superoxide dismutases.";
Gene 296:99-109(2002).
 STANDARD;
 74
159
163
 Similarity
 NCBI_TaxID=9483;
 NCBI_TaxID=9515;
 family.
 SODM CEBAP
 SEQUENCE
 Query Match
 Local
 QBHXP1;
 METAL
 SODM CEBAP
 Gene
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 1;
 88 ALKFNGGGHINHSLFWKNLAPYGSERATLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQ 147
 GSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPIIGVDIWEHAFYLQYKNVKPDYLA 203
 92 AIKFNGGGHVNHSIFWKNLAPSSEGGGEPPKGSLGSAIDAHFGSLEGLVKKMSAEGAAVQ 151
 87
 91
 28 TLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKLQS
 32 TLPDLPYDYGALEPAISGEIMQIHHQKHHQAYVTNYNNALEQLDQAVNKGDASTVVKLQS
 Gaps
 SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
ammalia, Butheria, Primates, Platyrrhini, Callitrichidae,
Callithrix.
cells and which are toxic to biological systems. CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2) COPACTOR: Binds 1 manganese ion per subunit (By similarity). SUBUNIT: Homotetramer (By similarity). SUBCELLULAR LOCATION: Mitochondrial matrix.
 4.
 MITOCHONDRION (BY SIMILARITY).
SUPERCXIDE DISMUTASE [MN].
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
 52.6%; Score 606; DB 1; Length 231; 60.2%; Pred. No. 7.2e-47;
 Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 21; Mismatches 51; Indels
 15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 2DBD5560A9E8AD7D CRC64;
 -> F (IN REF.
 198 AA
 MANGANESE
V -> F (IN
 Callithrix jacchus (Common marmoset)
 EMBL; AF061518; AAC24832.1;
EMBL; AC009991; AAF01529.1;
EMBL; AY072495; AAL66910.1;
EMBL; AY072495; AAL24289.1;
PIR; T50827; T50827.
HSSP; P04479; 1ASM.
InterPro; IPR001189; SODismutase.
Pfan; PF0081; sodfe (); 1.
Pfan; PF02777; sodfe (); 1.
ProDom; PD000475; SODismutase.
PRODOM; PD000475; SODismutase.
 PRT;
 25444 MW;
 al Similarity 60.2
115; Conservative
 204 AVWSVINYKEA 214
 212 NVWKVINWKYA 222
 STANDARD;
 231
231
103
192
196
 30
59
103
192
196
169
231 AA;
 Transit peptide.
 family.
 SODM_CALJA
 METAL
CONFLICT
SEQUENCE
 148
 Query Match
 152
 Best Local
 QBHXPO;
 CHAIN
 METAL
METAL
 CALJA
 Matches
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8 d 8 g SODM

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 86 QSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAA 145
 61 QPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLEAIKRDFGSFDKFKERLTAASVG 117
 146 VQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTHIPIIGVDIWEHAFYLQYKNVKPDYL 202
 118 VQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYL 177
 82
 9
 --- FUNCTION: Destroys radicals which are normally produced within the calls and which are toxic to biological systems.
--- CATALYMIC ACTIVITY: 2 superoxide + 2 H(+) = 0 (2) + H(2)0(2).
--- COPACTOR: Binds 1 manganese ion per subunit (By similarity).
--- SUBUNIT: Homoterzamer (By similarity).
---- SUBCELUIAR LOCATION: Mitcohondrial matrix (By similarity).
---- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL
 Gaps
 Cebus apella (Brown-capped capuchin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Cebinae, Cebus.
SEQUENCE FROM N.A.
MEDILINE=22271545; PubMed=12383507;
Fukuhara F., Tezuka T., Kageyama T.;
"Structure, molecular evolution, and gene expression of primate
 . 9
 52.5%; Score 605; DB 1; Length 198; 55.6%; Pred. No. 7.3e-47;
 54; Indels
 EMBL, AB087281, BAC20360.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PF00018, Sodfe: 1.
Pfam; PF0277; sodfe: 1.
PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODISMUtase; 1.
PROSITE, PS000088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
METAL
 MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
 15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)
 E7F8860B8C56F2CA CRC64;
 28; Mismatches
 198 AA
```

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 -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 Query Match 52.5%; Score 605; DB 1; Length 198; Best Local Similarity 55.6%; Pred. No. 7.3e-47; Matches 110; Conservative 28; Mismatches 54; Indels
 Oxidoreductase, Metal-binding, Manganese, Mitochondrion.
METAL 26 26 MANGANESE (BY SIMILARITY).
METAL 159 MANGANESE (BY SIMILARITY).
METAL 169 MANGANESE (BY SIMILARITY).
METAL 163 169 MANGANESE (BY SIMILARITY).
SEQUENCE 198 AA, 22248 MW, F7F8860B8C56F2CA CRC64;
 EMBL; AB087280; BAC20359.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
Pfam; PF02777; sodfe; 1.
PRINTS; PR01703; MNSÖDISMTASE.
PRODOM; PD000475; SODISMUTASE.
PROSTIE; PS00088; SOD.MN; 1.
[1]
SEQUENCE FROM N.A.
```

7 26 KHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKL 85 6; Gaps g

> $\stackrel{\triangleright}{\alpha}$ d à q ð

203 AAVWSVINYKEAEARLQA 220

|:|||: 178 KAIWNVINWENVTERYMA 195

Search completed: March 30, 2004, 17:14:38 Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 30, 2004, 17:09:18 ; Search time 26 Seconds
(without alignments)
821.328 Million cell updates/sec

Title: Perfect score:

US-09-727-855B-5 1153 1 MSVRASLSSVSRQTFVAPAA......AAVWSVINYKBAEARLQAAL 222 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |        | Description | superoxide dismuta | superoxide dismuta |        |       | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta |        |       |        | superoxide dismuta | superoxide dismuta | probable superoxid |        |        | superoxide dismuta | 3      | je.    |        | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | a)     | superoxide dismuta | _      | superoxide dismuta |  |
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| THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P |        |             | DSRTN              | I57023             | 151918 | DSHUN | T08181             | T50830             | T50827             | S65795             | T50828 | DSPMN | T06258 | 539492             | 803639             | T04072             | T04075 | T04312 | B48684             | T06801 | JC5122 | S03839 | T08045             | T50829             | T50831             | T47752             | S52721 | C48684             | T50070 | A48684             |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |        | DB          | <u>.</u>           |                    |        |       |                    |                    |                    |                    |        |       |        |                    |                    |                    |        |        |                    |        |        |        | N                  |                    |                    |                    |        |                    |        |                    |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |        | Length      | 222                | 222                | 222    | 222   | 231                | 237                | 231                | 204                | 228    | 240   | 231    | 233                | 228                | 231                | 231    | 231    | 233                | 231    | 221    | 235    | 228                | 205                | 240                | 241                | 218    | 232                | 218    | 233                |  |
| *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Query  | _           | 55.0               | 55.0               | 54.6   | 53.8  | 53.3               | 53.1               | 52.1               | 52.0               | 52.0   | 52.0  | 51.7   | 51.6               | 51.3               | 51.2               | 51.2   | 51.2   | 51.2               | 50.9   | 50.7   | 50.7   | 50.5               | 50.4               | 49.8               | 49.8               | 49.6   | 49.5               | 48.6   | 48.4               |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |        | Score       |                    | 634.5              | 629.5  | 620   | 614                | 612.5              | 601                | 009                | 009    | 009   | 296    | 595                | 592                | 590.5              | 590.5  | 5.065  | 290                | 587    | 584.5  | 584    | 582                | 581                | 574                | 574                | 572    | 570.5              | 260    | 558                |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Result | No.         | 1                  | 7                  | m      | 4     | Ω                  | 9                  | 7                  | <b>6</b> 0         | σ      | 10    | 11     | 12                 | 13                 | 14                 | 15     | 16     | 17                 | 18     | 19     | 20     | 21                 | 22                 | 23                 | 24                 | 25     | 26                 | 27     | 28                 |  |

1 MSVRASLSSVSRQTFVAPAAFQI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQT 58 

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57

119 GPLKKAJEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---L 175 

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| superoxide dismuta | probable superoxid | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta | superoxide dismuta |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T50832             | T09788             | A81688             | H71531             | B86498             | B72124             | B69709             | S22053             | DSBSNF             | JC1272             | AG1254             | A39223             | S48831             | S48832             | S20019             | AE1617             |
| ~                  | N                  | 7                  | 0                  | N                  | 0                  | ~                  | (1)                | 7                  | Ŋ                  | N                  | 0                  | 7                  | 7                  | 7                  | 0                  |
| 187                | 233                | 207                | 206                | 207                | 207                | 226                | 204                | 204                | 202                | 202                | 196                | 223                | 223                | 202                | 202                |
|                    | ۲.                 | 6.4                | 45.9               | 44.6               | 44.6               | 43.8               | 43.0               | 42.9               | 42.7               | 42.7               | 42.6               | 42.6               | 42.6               | 42.3               | 42.3               |
| 47.5               | 47                 | 4                  |                    |                    |                    |                    |                    |                    |                    |                    |                    | _                  |                    |                    |                    |
| 548 47.5           |                    |                    | 529.5              | 514.5              | 514.5              | 504.5              | 496                | 495                | 492                | 492                | 491.5              | 491.5              | 491.5              | 488                | 488                |

### ALIGNMENTS

| RESULT 1  BORING  Superoxide dismutase (EC 1.15.1.1) (Mn) precursor - rat  Cippecies: Rattus norvegicus (Doway rat)  Cipaceise: Rattus norvegicus (Doway rat)  Cipaceise: Alward, A.J.; Crapo, J.D.  Ribo, Y.S.; Howard, A.J.; Crapo, J.D.  Ribo, Y.S.; Howard, A.J.; Crapo, J.D.  Ribo, Y.S.; Howard, A.J.; Crapo, J.D.  A,Rocession: S21661  A,Rocleoule type: DNA  A,Reference number: S21661  A,Rocleoule type: DNA  A,Reference number: S0610; MUD: 857272; PIDN: CAA39937.1; PID: 957273  Ribo, Y.S.; Crapo, J.D.  Ribo, Y.S.; Crapo, J.S.; W.; Roce 634.5; D.S.; R.; Ratus predicted  Ribo, R.; Ratus predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Ribo, R.; Ratus Predicted  Rib |
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Query Match 54.6%
Best Local Similarity 54.3%
Matches 121; Conservative
 A; Molecule type: mRNA
A; Residues: 1-222 <CHU>
 A; Residues: 1-7 <MEY2>
 A; Gene: MnSOD
 R, Church, S.L.
 C; Genetics
 RESULT
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 A/Molecule type: DNA
A/Residues: 1-137, WM, 139-222 <-JON>
A/Rolecule type: DNA
A/Residues: 1-137, WM, 139-222 <-JON>
A/Rolecule type: DNA
A/Residues: 1-137, WM, 139-222 <-JON>
A/Rolecule type: DNA
A/Reference number: 836129
A/Rolecule type: mRNA
A/Residues: 1-22 <-SUNA
A/Rolecule type: mRNA
A/Residues: 1-22 <-SUNA
A/Residues: 1-24 <-SUNA
A/Residues: 1-24 <-SUNA
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A/Residues: 1-24 <-SUNA
A/Residues: 1-24 <-SUNA
A/Residues: 1-24 / Domain: transit peptide (mitochondrion) #status predicted <-NAT>
F/F50, 98,187,187/Binding site: manganese (Mis, His, Asp, His) #status predicted
 A; Accession: I57023
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: S78846; NID:g1037119; PIDN: AAB34899.1; PID:g1037120
B; Jones, P.L.; Kucera, G.; Gordon, H.; Boss, J.M.
A; Jones, P.L.; Kucera, G.; Gordon, H.; Boss, J.M.
A; Title: Cloning and characterization of the murine manganous superoxide dismutase-encod A; Reference number: JC4047; MUID:95180711; PMID:7875582
 3
 61 NGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGP 120
 NNLNATEEKYHEALAKGDVITQVALQPALKFNGGGHINHTIFWINLSPKGGGE---PKGE 116
 121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL--LTH 177
 1 MLCRAACSTGRRLGPVAGAAGS-RHKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYV 59
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 18-Jun-1999 C;Accession: 157023; JC4044; $36129; A25581 R;D15ilvestre, D.; Kleeberger, S.R.; Johns, J.; Levitt, R.C. Mamm. Genome 6, 281-284, 1995
 1 MSVRASLSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTXHHQTYV
 DB 2; Length 222;
 62; Indels
 178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 gene.
 mouse MnSOD g
PMID:7613035
 55.0%; Score 634.5; DB 2
55.6%; Pred. No. 6.5e-49;
iive 30; Mismatches 62
 A, Title: Structure and DNA sequence of the A, Reference number: 157023, MUID:95337589;
 Conservative
 Similarity
 124;
 09
 Query Match
 Best Loca
Matches
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RESULT 3

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superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - human
C.Species Homo sapiens (man)
C.Date: 04-Dec-1986 #sequence revision 06-Feb-1995 #text change 20-Apr-2000
C.Date: 05-Dec-1986 #sequence revision 56-Feb-1995 #text change 20-Apr-2000
C.Accession: 813162; 802272; 811756; 800356; 802230; 800663; A92447; 138033; A00520; A275
 A,Note: cross-reference GB:M34665 cited in paper is not correct
R;Wispe, J.R.; Clark, J.C.; Burhans, M.S.; Kropp, K.E.; Korfhagen, T.R.; Whitsett, J.A.
B;cohim. B;ophyga. Acta 994, 30-36, 1989
A;Title: Synthesis and processing of the precursor for human mangano-superoxide dismutass A;Reference number: S02772; MUID:89076921; PMID:2462451
 the bovine manganous superoxic
 C,Function:
A,Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 Biochim. Biophys. Acta 1087, 250-252, 1990
A;Title: Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of
A;Reference number: S13162; MUID:91027939; PMID:1699607
A;Accession: S13162
 116
 C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;1.24/Domain: transit peptide (mitochondrion) #status predicted <TNP>F;22-222/Product: superoxide dismusase (Mn) #status predicted <MAT>F;50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted
 61 NGLNAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGF 120
 121 LKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH 177
 09
 1 MLSRAACST-SRRLVPALSVLGSRQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYV 59
 C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct 1996 #sequence revision 15-Aug-1997 #text_change 21-Jul-2000
C;Accession: 151918; 164848; 164850
R;Meyrick, B.; Magnuson, M.A.
Am. J. Respir. Cell Mol. Biol. 10, 113-121, 1994
A;Tille: Identification and functional characterization of the bovine mangan A;Reference number: 151918; MUID:94121934; PMID:8292376
A;Accession: 151918
 1 MSVRASLSSVSRQTFVAPPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYV
 60 NNLNVAEEKYREALEKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PQGE
 Gaps
 A; Cross-references: GB:S67819; NID:9460572; PIDN:AAD14001.1; PID:94261701
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Kesidues: 'PROFAAST',1-222 <MEY1>
A;Cross-references: GB:L22092; NID:g498259; PIDN:AAA30655.1; PID:g498260
A;Accession: 164848
 A;Cross-references: GB:L22093; NID:g498261; PIDN:AAA30656.1; PID:g552330
A;Accession: 164850
 7 ;
 Length 222;
 Indels
 177 IPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTARYTA 219
 178 IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - bovine
 DB 2;
 63;
 54.6%; Score 629.5; DB 2 54.3%; Pred. No. 1.8e-48; tive 32; Mismatches 63.
 A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-7,'R' <MEY3>
 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A, Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen \varepsilon
 superoxide dismutase (EC 1.15.1.1) (Mn) precursor, mitochondrial (similarity) - leafy spv
 experimental
 C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted
 131 TSFGSLEGLVKKMSAEGAAVQGSGWVWLGLDKELKKLVVDTTANQDPLVTKGGSLVPLVG 190
 71 LEQLDQAVNKGDASAVVKLQSAIKFNGGGHVNHSIFWKNLAPVKEGGGEPPKGSLGGAID 130
 127 ESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPIIG 182
 124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWIGINPLTKKLEVTTTANQDPL---LTHIPI 180
 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
 63 NVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
 67 EESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIE 126
 20
 62
 C, Species: Raphanus sativus (radish)
C, Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
 7 LSSVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAA
 23 igsrsiotr------trpdipydysalepaisgeimoihhokhhoayvtnynna
 6 SLSSVSRQTFVAPAAFQI - RAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL
 Gaps
 Gaps
 C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>F;25-22/Product: superoxide dismutase (Mn) #status experimental <MAT>F;50,98,183,187/Binding site: manganese (His, His, Asp, His) #status experimental experimental control of the con
 16;
 10;
 Length 231;
 Length 222;
 61; Indels
 54; Indels
 A; Cross-references: EMBL: AF061333; NID: 93108344; PID: 93108345
 181 IGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEAEARLQA 220
 Query Match 53.8%; Score 620; DB 1; Best Local Similarity 53.6%; Pred. No. 1.3e-47; Matches 118; Conservative 31; Mismatches 61;
 ; Score 614; DB 2;
; Pred. No. 4.6e-47;
20; Mismatches 54
 A)Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-231 <KWO>
 183 VDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 222
 superoxide dismutase (EC 1.15.1.1) (Mn) - radish
 C,Accession: T08181
R,Kwon, S.I.; An, C.S.
submitted to the EMBL Data Library, April 1998
Superfamily: superoxide dismutase (Mn)
 53.3%;
 Query Match
Best Local Similarity 57.5%
Matches 122, Conservative
 A; Reference number: Z16401
 A; Accession: T08181
 64
 A; Gene: sod
 Genetics:
 RESULT 6
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-64, N', 66-222 <RES>
A;Residues: 1-64, N', 66-222 <RES>
A;Cross-references: EMBL:X59445; NID:g34708; PIDN:CAA42066.1; PID:g34709
B;Borgstahl, G.E.O.; Parge, H.E.; Hickey, M.J.; Beyer Jr., W.F.; Hallewell, R.A.; Tainer Cell 71, 107-118, 1992
A;Title: The structure of human mitochondrial manganese superoxide dismutase reveals a m
 aH
 A; Modecule type: mRNA
A; Residues: 1-64,'N', 66-222 < EMB>
A; Residues: 1-64,'N', 66-222 < EMB>
A; Cross-references: EMBL:X15132; NID:g34794; PIDN:CAA33228.1; PID:g34795
R; Ho, Y.S.; Crapo, J.D.
FRBS Lett. 229, 256-260, 1988
A; Title: Isolation and characterization of complementary DNAs encoding human manganese-cA; Reference number: S00356; MUID:88152250; PMID:2831093
 C:Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 G.
 manganese superoxide dismutase
 A;Residues: 1-154,'Q',156-222 <BEC>
A;Cross-references: EMBL:Y00472; NID:g34710; PIDN:CAA68533.1; PID:g34711
R;Barra, D.; Schinina, M.E.; Simmaco, M.; Bannister, J.V.; Bannister, W.H.; Rotilio, J. Biol. Chem. 259, 12555-12601, 1984
A;Title: The primary structure of human liver manganese superoxide dismutase.
A;Reference number: A92447; MUID:85030346; PMID:6386798
 A;Molecule type: protein
A;Reaidues: 25-65,'Q',67-111,'Q',113-132,'Q',134-147,150-154,'Q',156-222 <BAR>
R;St Clair, D.K.; Holland, J.C.
Cancer Res. 51, 939-943, 1991
 Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 25-222
 residues 25-222
 A;Molecule type: mRNA
A;Residues: 1-81, T', 83-222 <HO1>
A;Cross-references: EMBL:Y00985; NID:g36536; PIDN:CAA68791.1; PID:g36537
A;Hecks, K.
Nucleic Acids Res. 16, 6224, 1988
A;Title: Isolation of cDNAs encoding human manganese superoxide dismutase.
A;Reference number: S02230; MUID:88289364; PMID:3399391
 A; Molecule type: mRNA
A; Residues: 1-13, 'P', 15,'V', 17-122,'L', 124-222 < HEC>
A; Residues: 1-13, 'P', 15,'V', 17-122,'L', 124-222 < HEC>
A; Cross-references: EMBL:X07834; NID:g36517; PIDN:CAA30687.1; PID:g36518
A; Note: the authors translated the codon CTG for residue 123 as Arg
R; Beck, Y; Oren, R.; Amit, B.; Levanon, A.; Gorecki, M.; Hartman, J.R.
Nucleic Acids Res. 15, 9076, 1987
A; Title: Human Ms supercoxide dismutase CDNA sequence.
 A; Molecule type: mRNA
A; Residues: 1-81, T', 83-222 <WIS>
A; Residues: 1-81, T', 83-222 <WIS>
B; Coss-references: EMBL:X14322; NID:g34706; PIDN:CAA32502.1; PID:g34707
B; Etclair, D.K.
submitted to the EMBL Data Library, April 1989
A; Description: Nucleotide sequence of a human tumor MnSOD cDNA.
A; Reference number: S11756
 A;Reference number: A43483; MUID: 93008233; PMID: 1394426
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
R;Borgstahl, G.E.O.; Parge, H.E.; Tainer, J.A.
submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51016; PDB: 1ABM
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, A;Note: kidney recombinant form expressed in Escherichia coli R;Sussman, J.; Wagner, U.G.; Pattridge, K.A.; Ludwig, M.L.
submitted to the Brookhaven Protein Data Bank, November 1992
A;Reference number: A51304; PDB: 1MSD
 A;Title: Complementary DNA encoding human colon cancer n
A;Reference number: I38033; MUID:91105727; PMID:1988135
 A;Reference number: $00663; MUID:88067716; PMID:3684581
A;Accession: S00663
 Cross-references: GDB:119597; OMIM:147460
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C; Function:
 A; Molecule type: mRNA
 A; Accession: 138033
 A; Accession: S00356
 A;Accession: S11756
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Fuperoxide dismutase (EC 1.15.1.1) (Mn) - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Decies: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Mar-1999
C;Accession: 86795
C;Accession: 86795
E;Yuan, H.T.; Bingle, C.D.; Kelly, F.J.
Biochim. Biophys. Acta 1305, 163-171, 1996
A;Title: Differential patterns of antioxidant enzyme mRNA expression in guinea pig lung A;Reference number: 865793; MUID:96180320; PMID:8597602
A;Accession: 86795
A;Molecule type: mRNA
A;Residues: 1-204 < YUN>
C;Genetics:
 A,Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen C,Superfamily: superoxide dismutase (Mn)
 ä
 C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;52,100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted
 3;
 C;Superfamily: superoxide dismutase (mu)
C;Keywords: manganess; metalloprotein; mitochondrion; oxidoreductase
F;43,91,176,180/Binding site: manganese (His, His, Asp, His) #status predicted
 SYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKALEES 128
 61 KYQEALAKGDVTAQVALQPALKFNGGGHINHSIFWTNLSPNGGGE---PKGELLEAIKRD 117
 FGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPL---LTH1P11GVD1 185
 118 PGSFDKFKEKLTAVSVGVQGSGWGWLGFNKERGCLQIAACSNQDPLQGTTGLIPLLGIDV 177
 152 GSGWVWLGLDKELKKLVFDTTANQDPLVTKGGSLVPLVGIDVWEHAYYLQYKNVRPEYLK 211
 89
 9
 C;Species: Prunus persica
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C;Accession: T50828
R;Bagnoli, F.
submitted to the EMBL Data Library, October 1999
 9 SVSRQTFVAPAAFQIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEE
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 Length 204;
 52.0%; Score 600; DB 2; Length 228; 55.9%; Pred. No. 7.8e-46;
 Indels
 superoxide dismutase (EC 1.15.1.1) (Mn) 1 [similarity]
 61;
 52.0%; Score 600; DB 2;
55.4%; Pred. No. 6.7e-46;
ive 27; Mismatches 58;
 A;Reference number: Z25247
A;Accession: T50828
A;Status: preliminary; translated from GB/EMBL/DDBJ
 A; Cross-references: EMBL: AJ238316; PIDN: CAB56851.1
 ; Pred. No. 7.8e-
25; Mismatches
 178 WEHAYYLOLKNVRPDYLKAIWKVI 201
 186 WEHAFYLQYKNVKPDYLAAVWSVI
 Best Local Similarity 55.4 Matches 113; Conservative
 Best Local Similarity 55.9%
Matches 119; Conservative
 204 AVWSVINYKEA
 212 NVWKVINWKYA
 A;Molecule type: mRNĀ
A;Residues: 1-228 <BA
 A; Genome: nuclear C; Function:
 69
 129
 Query Match
 C, Genetics:
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Superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Arabidopsis thaliana superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Arabidopsis thaliana (mouse-ear crees)

C.Deceise: Arabidopsis thaliana (mouse-ear crees)

C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000

C.Accession: T50827

A.Title: Superoxide dismutase in Arabidopsis: an eclectic enzyme family with disparate : A.Reference number: 225246; MUID:98440686; PMID:976550

A.Accession: T50827

;Species: Euphorbia esula (leafy spurge)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C;Datession: 150830
R;Anderson, J.V.; Horvath, D.P.
submitted to the EMBL Data Library, March 2000
A;Description: Identification of mRNAs expressed in underground adventitious buds of EA;PREference number: Z25249
A;Accession: T50830
A;Reference number: Z25249
A;Accession: T50830
A;Reference number: Z25249
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A;Reference number: Z25249
A
 C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted
 2;
 1;
 124
 74 KALEQLHEATEKGDSSTVVKLQSAIKFNGGGHINHSIFWKNLAPVGEGGGELPHGSLGWA 133
 125 IEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH---IPII 181
 88 ALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQ 147
 GSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPIIGVDIWEHAPYLQYKNVKPDYLA 203
 64
 87
 91
 7 LSSVSRQTFVAPAAPQIRAKHŢ--LPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLN
 65 AAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKA
 28 TLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKEDVLTQVKLQS
 Gaps
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 DB 2; Length 237;
 Length 231;
 63; Indels
 52; Indels
 53.1%; Score 612.5; DB 2 56.3%; Pred. No. 6.4e-47; iive 25; Mismatches 63
 52.1%; Score 601; DB 2;
59.7%; Pred. No. 6.5e-46;
ive 21; Mismatches 52.
 182 GVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 A;Residues: 1721 cKLI>
A;Residues: 1231 cKLI>
A;Cross-references: EMBL:AF061518; PIDN:AAC24832.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MSD1
 Best Local Similarity 59.7
Matches 114, Conservative
 Conservative
 Similarity
 Query Match
Best Local Simi
Matches 120;
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 Query Match
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A,Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen c; Superfamily: superoxide dismutase (Mn)
C,Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted
 Superoxide dismutase (EC 1.15.1.1) (Mn) - Para rubber tree
C;Species: Hevea brasiliensis (Para rubber tree)
C;Species: Hevea brasiliensis (Para rubber tree)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C;Accession: 839492
R;Miao, Z.; Gaynor, J.J.
R;Miao, Z.; Gaynor, J.J.
A;Title: Molecular cloning, characterization and expression of Mn-superoxide dismutase
A;Reference number: 839492; MUID:94031306; PMID:9219064
 A;Genome: nuclear
(S.Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted
 ŝ
 116 GGGELPHGSLGWAIDADFGSLEKLIQLMNAEGAALQGSGWVMLALDKELKKLVVETTANQ 175
 52 HTKHHQTYVNGLNAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGS 111
 56 HOKHHQTYITNYNKALEQINDAIEKGDSAAVVKLQSAIKFNGGGHVNHSIFWKNLAPVRE 115
 112 EEATLSEGPLKKAIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQ 171
 137
 138 KFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLT-----HIPIIGVDIWEHAFYL 192
 142 KWNAEGAALQGSGWVWLALDKEAKRLSVETTPNQDPLVTKGSNLH-PLLGIDVWEHAYYL 200
 55
 51
 81
 A, Cross-references: EMBL: U72212; NID: 91622928; PIDN: AAB68035.1; PID: 91621627
 22 PAAARGVATFTLPDLPYDYGALEPAVSGEIMRLHHQKHHATYVANYNKALEQLDAAVSKG
 78 DVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAIBESFGSFEAFKK
 82 DASAVVHLOSAIKFNGGGHVNHSIFWKNLKPISEGGGEAPHGKLGWAIDEDFGSIEKLIK
 1 MSVRASLSSVSRQTFVAPAAF-----QIRAKHT--LPELPYAYDALEPSISKEIMTLH
 18 PAAFQIRAKHILPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNAAEESYSAAVGKE
 A;Cross-references: GB:L11707; NID:g348136; PIDN:AAA16792.1; PID:g348137 C;Function:
 18;
 . 9
 176 DPLVTKGPTLVPLLGIDVWEHAYYLQYKNVRPDYLKNIWKVMNWKYA 222
 51.6%; Score 595; DB 2; Length 233; ilarity 53.3%; Pred. No. 2.2e-45; Conservative 30; Mismatches 58; Indels
 Length 231;
 DPLLTH----IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA
 Indels
 Ouery Match 51.7%; Score 596; DB 2; I
Best Local Similarity 55.2%; Pred. No. 1.8e-45;
Matches 116; Conservative 23; Mismatches 65;
 201 QYKNVRPDYLTNIWKVVNWKYAGBEYEKVL 230
 OYKNVKPDYLAAVWSVINYKEAEARLQAAL
 Best Local Similarity
Matches 121; Conserv
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIA>
A;Residues: 1-231 <WUG>
 A; Accession: S39492
 193
 172
 A; Gene: SOD3.1
 Query Match
 C; Genetics
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 C,Dāte: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999
C;Accession: $18343; $15560
C;Accession: $18343; $15560
E;Avorg-Vega, L.; Burke, J.J.; Allen, R.D.
Plant Mol. Biol. 17, 1271-1274, 1991
A;Title: Isolation and sequence analysis of a cDNA that encodes pea manganese superoxide A;Reference number: $18343; MUID:92032795; PMID:1932701
 A)Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen C;Superfamily: superoxide dismutase (Mn)
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; syloreductase
F;1-36/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;37-240/Product: superoxide dismutase (Mn) #status predicted <MAT>
F;64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted
 9
 DINFGSLEALVQKANAEGAEAQGSGWVWLALDKELKKLVVETTANQDFLVTKGPTLVPLL 186
 56 HQTYVNGLNAABESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEAT 115
 116 LSEG---PLKK----AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTŢŢ 168
 67 ALEQIHDAISKGDAPTVAKIHSAIKFNGGGHINHSIFWKNLAPVREGGGEPPKGSLGWAI 126
 EESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPII 181
 55
 68
 7 VSRRTLATGLGFRQQLRGLQTFSLPDLPYNYGALEPAISGDIMQLHHQNHQTYVTNNNK 66
 65
 C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Apr-2000
C;Accession: T06258
 69 HQTYITUYNKALBQLHDAVAKADISTTVKLQNAIKFNGGGHINHSIFWKNLAP-----
 4 RASLSSVSRQ-----TFVAPAAFQIRAKH--TLPELPYAYDALEPSISKEIMTLHHTKH
 10 VSRQTFVAPAAF -- QIRAKHT -- LPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNA
 26; Gaps
 A;Cross-references: EMBL:X60170; NID:g20901; PIDN:CAA42737.1; PID:g20902
 169 ANODPLLTH----IPIIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 182 ANODELVTKGASEVPLLMIDVWEHAYYLOYKNVRPDYLKNIWKVINWKHA 231
 Length 240;
 51; Indels
 superoxide dismutase (BC 1.15.1.1) (Mn) precursor - garden pea
C;Species: Pisum sativum (garden pea)
 superoxide dismutase (EC 1.15.1.1) (Mn) precursor - wheat
 Query Match 52.0%; Score 600; DB 1; Best Local Similarity 54.3%; Pred. No. 8.4e-46; Matches 125; Conservative 28; Mismatches 51.
 R,Wu, G.; Robertson, A.J.; Wilen, R.W.; Gusta, L.V. submitted to the EMBL Data Library, September 1996 A; Reference number: 21551 A; Accession: T06258 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
 GVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 GIDVWEHAYYLQYKNVRPDYLKNIWKVINWKYA 219
 Query Match
Best Local Similarity
 A; Molecule type: mRNA
A; Residues: 1-240 < WON>
 A; Accession: S18343
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Mismatches Pred. No.

63 67

---TLPELPYAYDALEPSISKEIMTLHHTKHHOTYVNGL

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A; Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen a
 C.Species: Oryza sativa (rice)
C.Jate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Apr-2000
C.Jacession: T04079
C.Jacession: T04079
C.Jacession: T04079
C.Jacession: T04079
C.Jacession: T04079
Submitted to the EMBL Data Library, December 1994
A.Description: Rice manganese superoxide dismutase are encoded by multigene family.
A.Reference number: 215187
 64 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
 68 NKALEQLDAAVAKGDAPAIVHLOSAIKFNGGGHVNHSIFWNNLKPISEGGGDPPHAKLGW 127
 8 SRKTLAAAALPLAAAAARGVTTVALPDLPYDYGALEPAISGEIMRLHHOKHHATYVANY
 124 AIBESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IP
 A;Residues: 1-231 <PAN>
A;Residues: 1-231 <PAN>
A;Cross_references: EMBL:L34039; NID:g601870; PIDN:AAA57131.1; PID:g601871
 probable superoxide dismutase (EC 1.15.1.1) (Mn) 2 precursor - rice
 180 IIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 188 LLGIDVWEHAYYLQYKNVRPDYLSNIWKVNNWKYA 222
 A;Accession: T04075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
PAAFQIRAKH-
 118; Conservative
 11 SROTFVA---
 Best Local Similarity
 A;Gene: rmsod2
A;Genome: nuclear
 C; Function:
 Matches
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 probable superoxide dismutase (EC 1.15.1.1) (Mn) precursor - rice C;Species: Oryza sativa (rice) C;Species: Oryza sativa (rice) C;Species: Oryza sativa (rice) C;Apr.1999 #sequence_revision 23-Apr.1999 #text_change 20-Apr-2000 C;Accession: 104072 A;Pan, S.M.; Chen, J.C. Submitted to the EMBL Data Library, December 1994 A;December: Rice manganese superoxide dismutase are encoded by multigene family. A;Reference number: 215187 A;Reference number: 215187 A;Reference number: 215187 A;Molecule type: mRNA A;Residues: 1-231 c,Pan> A;Residues: 1-231 c,Pan> A;Residues: 1-231 c,Pan> A;Residues: 1-231 c,Pan> A;Genetics: EMBL:L34038; NID:g601868; PIDN:AAA57130.1; PID:g601869 C;Genetics: A;Genetics: A;Genet
 3
 66 AEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKKAI 125
 BESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IPII 181
 10 VSRQTFVAPAAF--QIRAKHT--LPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGLNA 65
 99
 7 VSRRTLATGLGFRQQLRGLQTFSLPDLPYDYGALEPAISGDIMQLHHQNHHQTYVTNYNK
 Gaps
 Length 228;
 51.3%; Score 592; DB 2; Length 22 54.0%; Pred. No. 4e-45; ive 30; Mismatches 60; Indels
 GIDVWEHAYYLQYKNVRPDYLKNIWKVMNWKYA 219
 GVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 Best Local Similarity 54.0
Matches 115; Conservative
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C; Superfamily: superoxide dismutase (Mn)
C; Superfamily: superoxide dismutase (Mn)
C; Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F; 1-27/Domain: transit peptide (mitochondrion) #status predicted <TND>
F; 28-231/Product: superoxide dismutase (Mn) #status predicted <MAT>
F; 55, 103, 192, 196/Binding site: manganese (His, His, Asp, His) #status predicted
 68 NKALEQLDAAVAKGDAPAIVHLOSAIKFNGGGHVNHSIFWNNLKPISEGGGEPPHAKLGW 127
 124 AIEESFGSFEAFKKKFNADTAAVQGSGWGWLGLNPLTKKLEVTTTANQDPLLTH----IP 179
 128 AIDEDFGSFEALVKKMSAEGAALQGSGWVWLALDKEAKKLSVETTANQDPLVTKGANLVP 187
 NAAEESYSAAVGKEDVLTQVKLQSALKFNGGGHINHSLFWKNLAPYGSEEATLSEGPLKK 123
 SRQTFVA---PAAFQIRAKH----TLPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL 63
 Gaps
 Indels 11;
 Length 231;
 62;
 DB 2;
 180 IIGVDIWEHAFYLQYKNVKPDYLAAVWSVINYKEA 214
 Query Match
51.2%; Score 590.5; DB 2
Best Local Similarity 54.9%; Pred. No. 5.6e-45;
Matches 118; Conservative 24; Mismatches 62
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A,Description: catalyzes the dismutation of 2 molecules of peroxide radical to dis C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese, metalloprotein; mitochondrion; oxidoreductase
F;2-7)Domain: transit peptide (mitochondrion) #status predicted <TNP>F;28-231/Product: superoxide dismutase (BC 1.15.1.1) (Mn) #status predicted <MAT>F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted